



"Replacement Sheet"

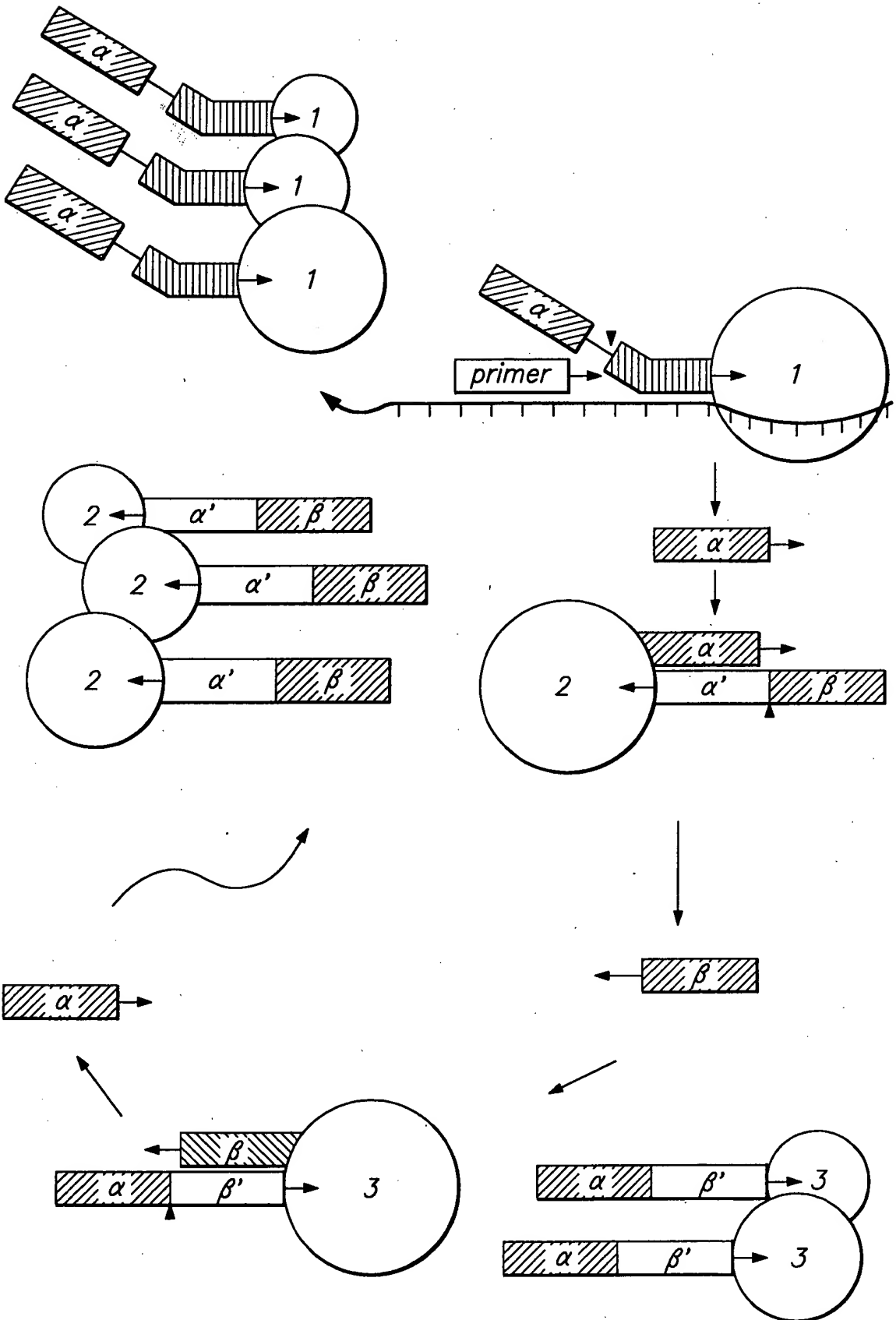
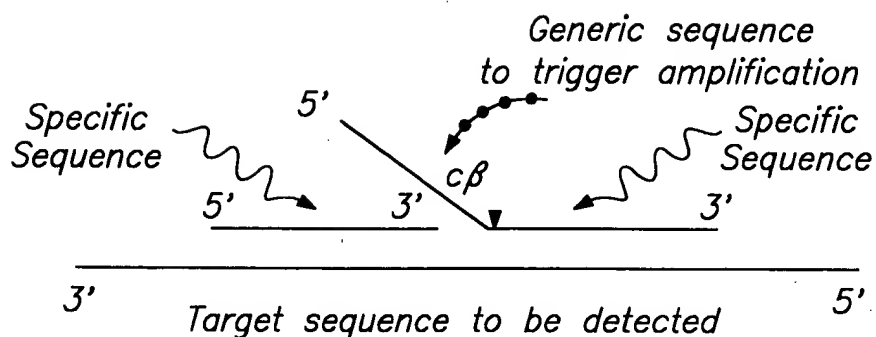
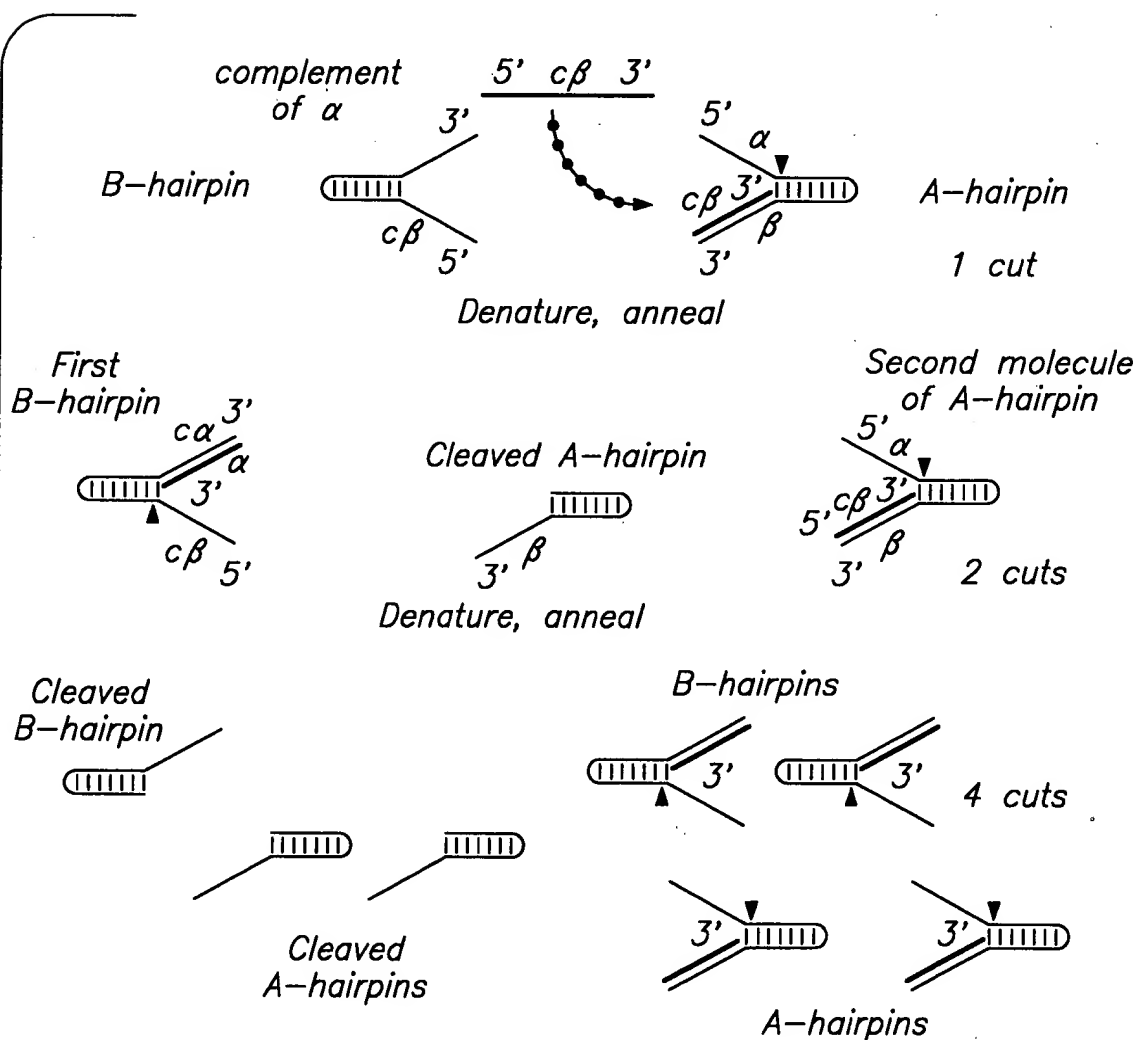


FIG. 1A

**FIG. 1B**



**PART ONE: TRIGGER REACTION**



**PART TWO: DETECTION REACTION**

FIG. 2A

MAJORITY [SEQ ID NO:7]	ATGXXGGCGATGCTTCCCTCTTGAGCCGAAGGCCGGCTCCTCCTGCTGGACGGCCACCACTGGCGT	
DNAPTAD [SEQ ID NO:1]	..AG..G.....G.....G.....	70
DNAPTFL [SEQ ID NO:2]	.....G.....C..G.....	67
DNAPTTH [SEQ ID NO:3]	..GA.....G.....A.....	70
MAJORITY	ACGGCAGCTTCTTGGCGCTGAAGGGCTCAGCACCAGCCGGGGCAACCGTGCAGGGCTCTACGGCT	
DNAPTAD	.....GA.....G.....G.....G.....	140
DNAPTFL	.....T.....G.....C.....C..T.....	137
DNAPTTH	.....G.....G.....	140
MAJORITY	CGCGAAGAGCCTCCTCAAGGCCCTGAAGGAGGACGGGACXXGGGGTGXTCGTGCTTTGAGGCCAAG	
DNAPTAD	.....G.....G.....A.....	207
DNAPTFL	..A.....GT..T.....	204
DNAPTTH	.....T..AA..G..GT.....	210
MAJORITY	GGCCCTCCTCGCCGACGAGGCTACGAGGCTACAAGGGGGGGCCGCCACCCCGAGGACTTC	
DNAPTAD	.....G..GG.....G.....	277
DNAPTFL	.....G.....G.....	274
DNAPTTH	.....GA.....G.....C.....C.....	280
MAJORITY	CGCGGAGCTGGCGCTGATCAAGGAGCTGCTGAGCCTCCTGGGGCTTGGGGCCTCGAGGTCGCCGGCTA	
DNAPTAD	.....A.....G.....G.....	347
DNAPTFL	.....G.....T.....A..C.....T..G..G.....T.....	344
DNAPTTH	.....T.....T..A..G.....	350

MAJORITY	[SEQ ID NO:73]	CGAGGGGAGGAGGTGCTGGCCACCCCTGGCCAGAAGCGCGAAAGAGGGCTACGAGCTGGCATCTC	
DNAPTAD	[SEQ ID NO:13]	.....C.....G.....	417
DNAPTFL	[SEQ ID NO:23]	T.....G.....CG.....	414
DNAPTTH	[SEQ ID NO:33]	.....T.....G.....	420
MAJORITY		ACGGCCGAGCGGACCTCTACGAGCTCTTCCGAGCGCATCGGGCTCCTCGACCCGAGGGGTACCTCA	
DNAPTAD		.....AAA.....T.....	487
DNAPTFL		T.....	484
DNAPTTH		.....A.....G.....G.....	490
MAJORITY		TGACCCCGGGCTGGCTTGGGAGAAGTACGGCCCTGAGCCCGGAGCACTGGTGGACTACCGGGCCCTGGC	
DNAPTAD		.....C.....A.....	557
DNAPTFL		.....AC.....	554
DNAPTTH		.....A.....G.....T.....C.....T.....	560
MAJORITY		GGGGAGCCGCTCGGACAACCTCCGGGGGTGAAGGGCATCGGGGAGAAGACGGCCGXGAAGCTCCTCXAG	
DNAPTAD		C.....GAG.....T.....	627
DNAPTFL		.....G.....T.....A.....G.....	624
DNAPTTH		.....	630
MAJORITY		GAGTGGGGGAGCGCTGGAAAACCTCCTCAAGAACTGGACGGGCTGAAGCCCGC...CTTCGGGGAGAGA	
DNAPTAD		.....GC.....	694
DNAPTFL		.....T.....C.....A.....	691
DNAPTTH		A.....A.....A.....A.....G.....	700



FIG. 2C

MAJORITY	[SEQ ID NO:7]	TCGAGGCCACATGGAXGACCTGAXGCTCTGCTGGAGCTXTGCCAGGTGGCGACGACCTGGCCCTGGA	
DNAPTAD	[SEQ ID NO:1]	...T.....C..T...A.....C..GG..A.....	764
DNAPTFL	[SEQ ID NO:2]	...GGG...G..C...GCC..T...C..A...T.....A...T.....	761
DNAPTTH	[SEQ ID NO:3]	...A.....C...A.....C..G.....T.....C...G.....C.....	770
MAJORITY		GCTGACTTCGCCAAGXGGCGGAGCGCGACCGGAGGGGCTTAGGGCTTCTGAGAGGCTGGACTT	
DNAPTAD		...A.....A.....A.....A.....T.....T.....	834
DNAPTFL		...GG..G..C..C..GACA..A...T.....T..GC...T...C..T.....	831
DNAPTTH		...C...C...G..G.....C.....C.....C.....	840
MAJORITY		GGCAGCCTCCTCCACGAGCTCGGCTCCTGGAGGCGCCCAAGGCCCTGGAGAGGCCCCCTGGCCCGCG	
DNAPTAD		...T.....AA.....G.....G.....GCCA.....T.....	904
DNAPTFL		...A.....G.....G.....GCCA.....T.....	901
DNAPTTH		...G.....GCCG.....	910
MAJORITY		CGCAGGGGCTTGGTGGCTTGTCTTCCGCGCCGAGGCCATGTGGCGGAGCTCTGGCCCTGGC	
DNAPTAD		...G.....AG.....T.....	974
DNAPTFL		...T..T.....TC..T.....T.....	971
DNAPTTH		...G.....G.....AAA.....	980
MAJORITY		CGCCGCCAGGGAGGGCCGGCTGCACCGGCGACGAGACCCCTTAXGGGCTXAGGGACCTXAAGGAGGTG	
DNAPTAD		...G.....C..C..G..T..A..AA..C...C.....G.....C.....	1044
DNAPTFL		...T..G..GT.....G..CC...T.....A.....G.....G.....T.....G.....	1041
DNAPTTH		...TG.....C.....G.....G.....GGC...G..A..A.....C.....C.....	1050

FIG. 2D

MAJORITY	ESQ ID NO:7J	GGGGXCTGCTGCCAAGGACCTGGCGTTTGGCCCTGAGGAGGGCCCTXGACCTCTGCGCGGGAGC	
DNAPTAD	ESQ ID NO:1J	.....G..T.....A.....AG.....C.....A.....T..G.....CC.....C.....	1114
DNAPTFL	ESQ ID NO:2J	.....AA.....G.....G.....C.....C.....G.....T..C.....A..A.....	1111
DNAPTTH	ESQ ID NO:3J	.....C.....C.....C.....C.....TC.....G..A.....G.....	1120
MAJORITY		ACCCATGCTCTCGCTACCTCTGAGCCCTCCAACACACCCCGAGGGGTGGCCCGGCGCTACGG	
DNAPTAD		.....T.....T.....T.....T.....T.....T.....T.....T.....T.....	1184
DNAPTFL		.....G.....T.....T.....T.....T.....T.....T.....T.....T.....	1181
DNAPTTH		.....G.....G.....G.....G.....G.....G.....G.....G.....G.....	1190
MAJORITY		GGGGAGTGGACGGAGGAXGCGGGGAGCGGGCCCTCCTXTCGAGAGGCTCTCCXGACCTXXXGGAG	
DNAPTAD		G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....	1254
DNAPTFL		.....T.....T.....T.....T.....T.....T.....T.....T.....T.....	1251
DNAPTTH		.....C..G..G..G..C.....C..G.....CAT..G.....CCTTA..	1260
MAJORITY		CGCGTGAAGGGGAGGAGGCTCCTTGCTTACCAAGAGCTGGAGAGCCCTTTCGGGGTCTCG	
DNAPTAD		A..G.....A.....A..A..AC..C..G.....G.....G.....GCT.....	1324
DNAPTFL		.....A.....A.....A.....A.....G.....G.....G.....GT.....	1321
DNAPTTH		.....C.....C.....A.....C.....C.....A.....C.....	1330
MAJORITY		CCACATGGAGGGCAGCGGGGTXGCGCTGGAGCTGGCTACCTCAGGCGCCTXTCCTGGAGGTGGCGGA	
DNAPTAD		.....G.....G.....G.....G.....T.....AG.....T..G.....C.....	1394
DNAPTFL		.....GG.....C.....C.....C.....C.....C.....C.....A..C.....	1391
DNAPTTH		.....C.....A.....A.....T.....T.....T.....C..T.....	1400

FIG. 2E

MAJORITY [SEQ ID NO:7]		GGAGATCGGGGGCTCGAGGAGAGGTCTTCGGCTGGCGGGCAGCCCTCAACCTCACTCCGGGAC	
DNAPTAA	[SEQ ID NO:12]	.....GC.....CG.....	1464
DNAPTFL	[SEQ ID NO:23]	...G.G...AG..G.....	1461
DNAPTTH	[SEQ ID NO:33]	.....	1470
MAJORITY		CAGCTGGAAAGGCTGCTCTTGACGAGCTXGGGCTTCGGCCATCGGCAAGACGGAGAAGACXGCCAAGC	
DNAPTAA		.....G.....A.....	1534
DNAPTFL		.....GC.....G..C..G..T.....	1531
DNAPTTH		.....TA.....T.G..G.....C.A.....A.....	1540
MAJORITY		GCTCGACCAAGCGGGGGCTGCTGGAGGGCTXCGXAGGGCCACCCGATGCTGAGAAGATGCTGCAGTA	
DNAPTAA		.....G.....G.....C..C.....	1604
DNAPTFL		.....T.....G..A.....GGG.....	1601
DNAPTTH		.....G.....A..G.....C.....C.....C.....	1610
MAJORITY		CGGGAGCTCAGCAAGCTCAAGAACAGCCTACATXGAGCGGCTGCCXGCTGCTGCACCCCAAGACGGGC	
DNAPTAA		.....G.....G.....T.....T.....G.A.....A.....	1674
DNAPTFL		.....A.....A.....C.G..G.....A..C.....	1671
DNAPTTH		.....G.G.....C..AAG.....G.....	1680
MAJORITY		CGGCTCGACACCGGCTTCAACGAGACGGCCACGGCCAGGCTTAGTACCTCGACCCCAACCTGC	
DNAPTAA		.....A.....T.....C.....	1744
DNAPTFL		...G.....C.....TCG.....	1741
DNAPTTH		.....G.....	1750

FIG. 2F

MAJORITY	[SEQ ID NO: 7]	AGACATCGCCGTCGCGACGCCXCTGGGCGAGGATCCCGCGGCCCTTGTGGCGAGGAGGXTGGT	
DNAPTAD	[SEQ ID NO: 1]	.....G..T..G.....A..C.....G...C.	1814
DNAPTFL	[SEQ ID NO: 2]	.....G.....T.....C..C.....A.....C.....	1811
DNAPTTR	[SEQ ID NO: 3]	.....CT.....C.....T.....G.....	1820
MAJORITY		GTGCTGGCCGTGACTATAGCCAGATAGAGCTCGGGCTCTGGCCACCTCTCGGGCGACGAACTG	
DNAPTAD		A.....T.....A.....G.....C.....	1884
DNAPTFL		.C.....T..T.....C.....T.....T.....	1881
DNAPTTR		.....G.....C.....A.....	1890
MAJORITY		ATCGGGCTCTCAAGAGGGGAGGACATCAACACCAGACCGCAGCTGGATGTTGGCGCTCCGCCCGG	
DNAPTAD		.....G.....GG.....G.....	1954
DNAPTFL		.....T.....A.....T.....C.....	1951
DNAPTTR		..A.....A.....A.....	1950
MAJORITY		AGCGCGTGGACCCCTGATGGCGCGCGGCGCAAGCATTGGGGTCTCTACGGCATGTCGG	
DNAPTAD		.....A.....G.....G.....	2024
DNAPTFL		.A..G..A.....T.....G.....G.....	2021
DNAPTTR		.....G..G..G.....C.....	2030
MAJORITY		CCACCGCCTCTCCAGGAGCTGCCATCCCTACGAGGAGGGGTGGCCTCATGAGCGCTACTTCAG	
DNAPTAD		.....A.....T.....T.....CCA.....T.....	2094
DNAPTFL		.....GG.....T.....T.....	2091
DNAPTTR		...TA..G.....T..A.....A	2100

FIG. 2G

MAJORITY [SEQ ID NO:7]			ACCTTCGGCAAGCTGGGGCGCTGATTGAGAGACCCTCGAGGAGGGAGAGGGCGGGTACGTGAGA	
DNAPTAA	[SEQ ID NO:13]	2154	.....	
DNAPTFL	[SEQ ID NO:23]	2151	.....A.....GG.....G.....T.....	
DNAPTTH	[SEQ ID NO:33]	2170	.....A.....A.....G.....A.....C.....A.....	
MAJORITY			CCCTCTGGGGCGGGCGCTACGTGCGCGACCTCAAGCGCGGGTGAAGAGCGTGGGGAGCGCGCGGA	
DNAPTAA		2234	.....C.....A.....AG.G.....	
DNAPTFL		2231	.....T.....	
DNAPTTH		2240	.....AA.AA.....CA.....C.....	
MAJORITY			GGGATGGGCTTCAACATGGCGCTCGAGGGCACCAGCGGACCTCATGAAGCTGGGCAIGGTGAAGCTG	
DNAPTAA		2304	.....T.....	
DNAPTFL		2301	.....G.....CG..T	
DNAPTTH		2310	.....C.....	
MAJORITY			TTGGCGCGGCTXCAGGAATGGGGCGAGATGCTCTXCAGGTCACAGCAGAGCTGGTCTCGAGGCCC	
DNAPTAA		2374	.....A.....GG.....T.....	
DNAPTFL		2371	.....T.....G.....TT.G.....G.....	
DNAPTTH		2380	.....G.G.G.....G.....G.....CG.....G.....	
MAJORITY			GCAAGAGCGGGCGGAGCGXGCTGGCGCCTTTGGCAGAGAGCTCATGGAGGGGTCTATGCCCTGGCGCT	
DNAPTAA		2444	.....A.....A.....CG.....CGCG.....G.....	
DNAPTFL		2441	.....G.C.....AG.A.....G.....GAG..	
DNAPTTH		2450	.....C.C.....C.A.....G.....AA.C.....C.....	

## FIG. 2H

MAJORITY	[SEQ ID NO:7]	GGCCCTGGAGGTGGAGGTGGGATGGGGAGGACTGGCTCTGGGCAAGGAGTAG
DNAPTAA	[SEQ ID NO:1]	.....A.....GA
DNAPTFL	[SEQ ID NO:2]	.....CG.....
DNAPTH	[SEQ ID NO:3]	.....T.....GT...

FIG. 3A

MAJORITY	[SEQ ID NO:8]	MXAMLPLFEPRGRVLLVDGHLAYRTFFALKGLTTSRGEPUQAVYGFAKSLKALKEDG-DVVXVVFDAK	
TAQ PRO	[SEQ ID NO:4]	.RG.....H.....	69
TFL PRO	[SEQ ID NO:5]	.....	68
TTR PRO	[SEQ ID NO:6]	.E.....YK.F.....	70
MAJORITY		APSFREAYEAYKAGRPTPEDFPROLALIKELVDLGLXRLVPGYEADDVLATLAKKAKEGYEVRIL	
TAQ PRO		.....GG.....A.....S.....	139
TFL PRO		.....V.....F.....R.....	138
TTR PRO		.....FT.....	140
MAJORITY		TADRDLYLLSDRIAVLHPEGYLLTPAWLWEKYGLRPEQWVDYRALXGDPSONLPGVKIGEXTAKLLX	
TAQ PRO		..K.....H.....D.A.....T.E.....R..E	209
TFL PRO		.....E..I.....Y.....A.....I.....QR.IR	208
TTR PRO		.....V..V.....H...E.....F..V.....L...K	210
MAJORITY		EWGSLLENLKNLDRVKP-XXREKIXAHMEDLXLSXLSXVRTDLPLEVDFAXRREPDRGLRAFLERLEF	
TAQ PRO		.....A.....L..Al...L...D..K..WD.AK.....K.....R.....	278
TFL PRO		.....FOH.O...SL..LQ.G..A.A..RK..Q.H.....GR..T.NL.....	277
TTR PRO		.....ENV...K.L...R..LE..R.....L.OG.....	280
MAJORITY		GSLHFEGLLEXPKALEAPWPPEGAFVGFVLSRPERMMAELLALAARRXGRVHRAXDPLXGLROLKEV	
TAQ PRO		.....S.....K.....D.....G.....PE.YKA.....A	348
TFL PRO		.....G..A.....L..SF.....G.WE..I..Q...R.....G.	347
TTR PRO		.....A.AP.....K.....G.D.....A...A..K.....	350

FIG. 3B

MAJORITY	CSEO ID NO:8J	RGLLAKDLAVLALREGLDXPDDPMLLAYLLDPSNTTPEGVARRYGGEWTEADAGERALLSERLFXNLXX	
TAQ PRO	CSEO ID NO:4J	.....S.....G.P.....E.....A.....A.....A.....WG	418
TFL PRO	CSEO ID NO:5J	.....I.....F.E.....F.....A.....OT.KE	417
TTR PRO	CSEO ID NO:6J	.....S.....V.....AH.....HR..LK	420
MAJORITY	RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRRLEEEVFRLAGHPFNLNSRD		
TAQ PRO	.....R..R..A.....R.....A..A.....A.....	488	
TFL PRO	.....K.....E.....R.....EA.V.Q.....	487	
TTR PRO	.....K.....H.....L.....	490	
MAJORITY	QLERVLFDLGLPAIGKTEKTGKRSTSAVLEALREAHPIVEKILQYRELTKLKNTYIDPLPXLVHPRTG		
TAQ PRO	.....DR.....S.....D.I.....	558	
TFL PRO	.....R..L..Q.....H.....V.....S.....	557	
TTR PRO	.....R..L..Q.....H.....V.....S.....	560	
MAJORITY	RLHTRFNQATATGRSSSDPNLONI PVRTPLGQRI RRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL		
TAQ PRO	.....L.....L.....	628	
TFL PRO	.....V..V.....	627	
TTR PRO	.....A..A.....	630	
MAJORITY	IRVFQEGRDIHTOTASWMTGVPPEAVDPLMRRAAKTINFGVLYGMSAHRLSQELAI PYEEAVAFIERYFO		
TAQ PRO	.....E.....R.....G.....Q.....	698	
TFL PRO	.....S..G.....G..S.....	697	
TTR PRO	.....K.....V.....	700	



FIG. 3C

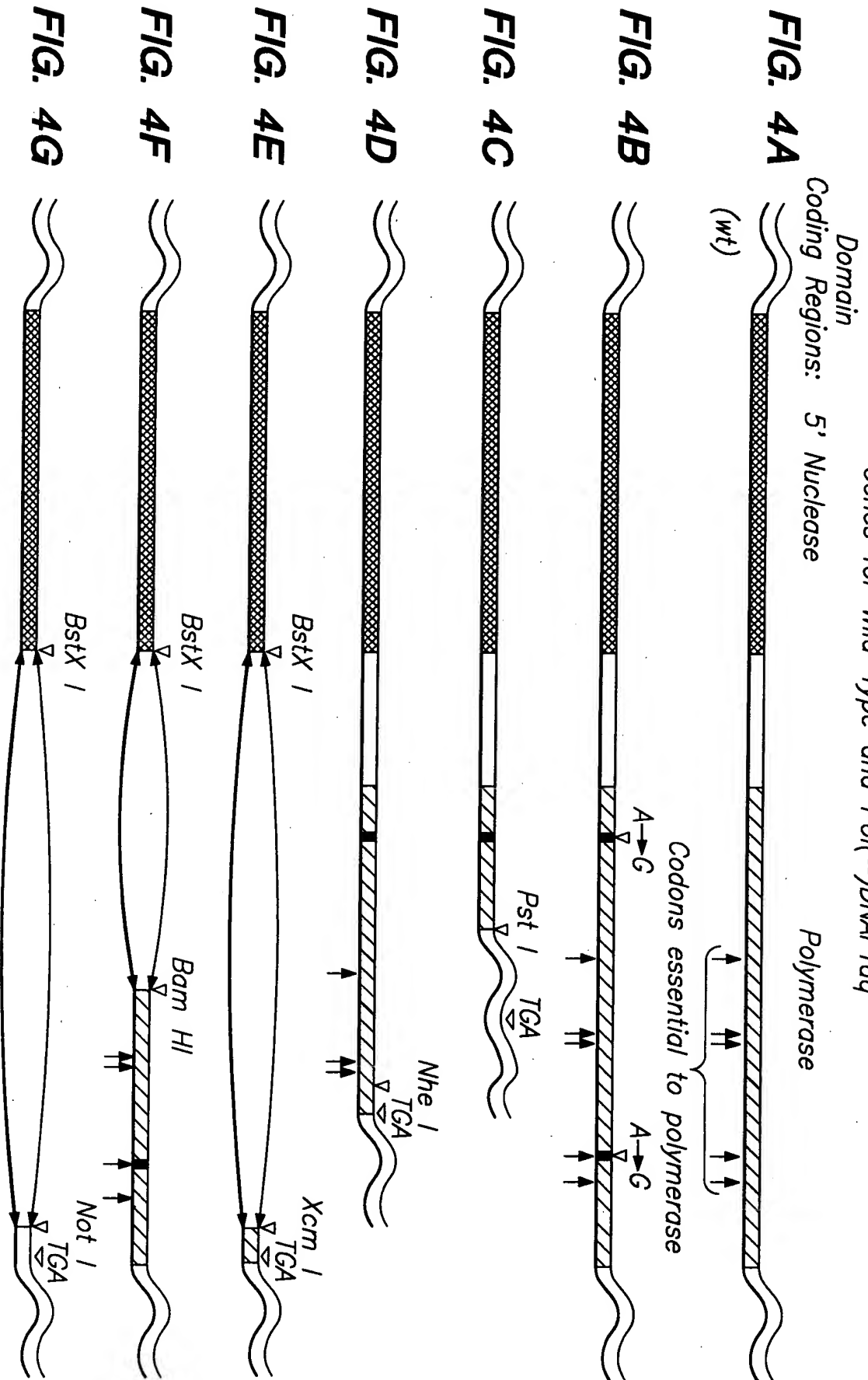
MAJORITY [SEQ ID NO: 83] SFPKVRAWI EKTLEGGRRRGVETLFGRRRYVPDINARVKSVREAE RMAFNMPVQGTAA DLMKLAMVKL

TAQ PRO	[SEQ ID NO: 43]	.....	E	.....	768
TFL PRO	[SEQ ID NO: 53]	Y.....	G	.....	767
TTH PRO	[SEQ ID NO: 63]	.....	K	.....	770

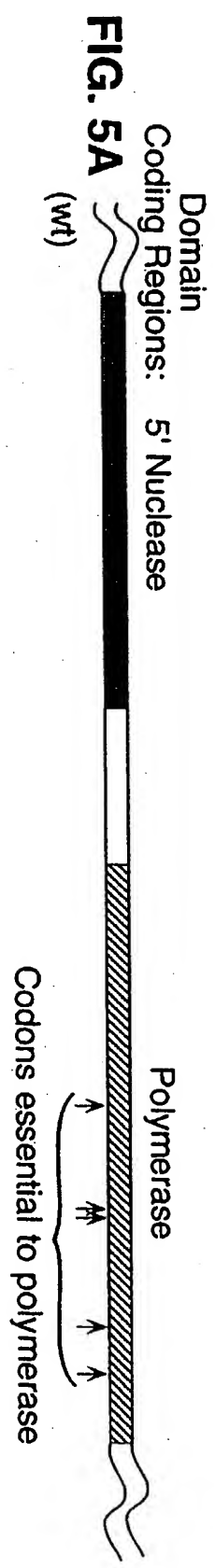
MAJORITY FPRXEMGARM LQVHDELVL EAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX

TAQ PRO	.....	E	.....	E	A	R	.....	833
TFL PRO	.....	Q	L	.....	D	R	.....	831
TTH PRO	.....	R	.....	L	QA	E	.....	835

Genes for Wild-Type and Pol(-)DNAPTaq



Genes for Wild-Type and Pol(-) DNAPTII



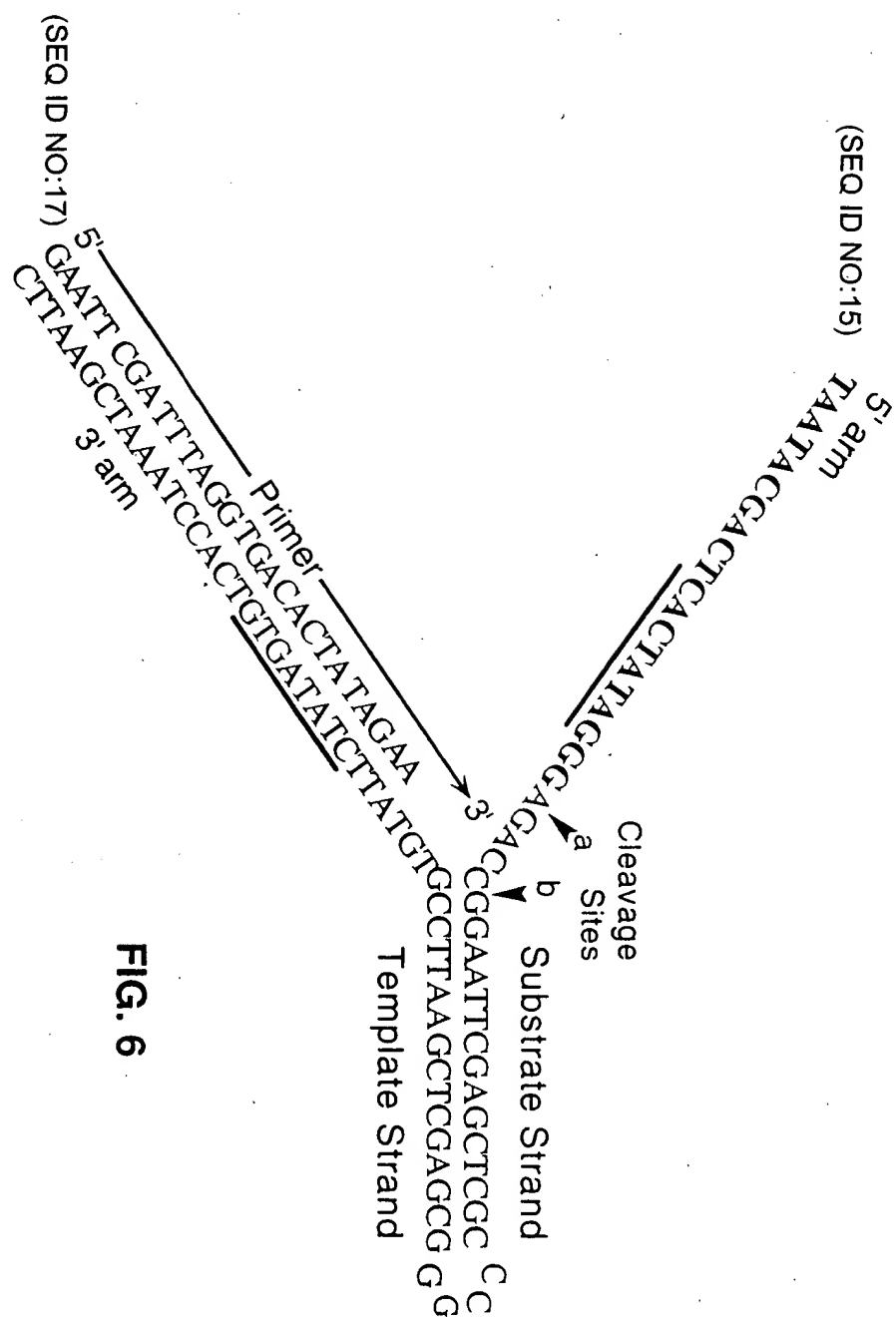


FIG. 6

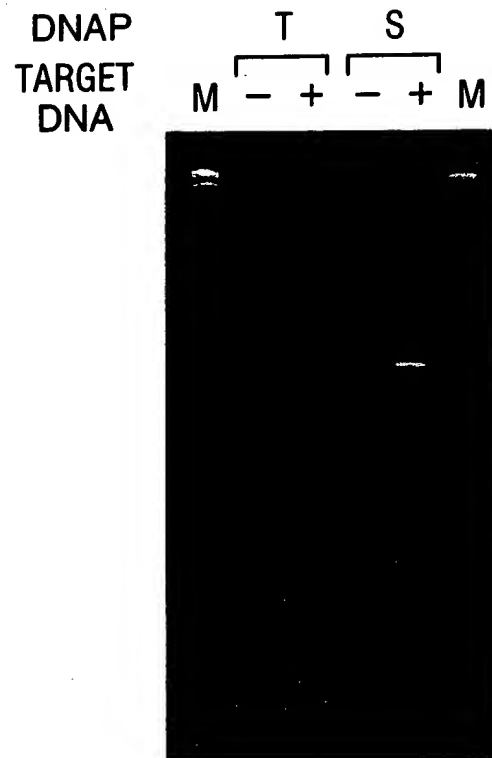


FIG. 7

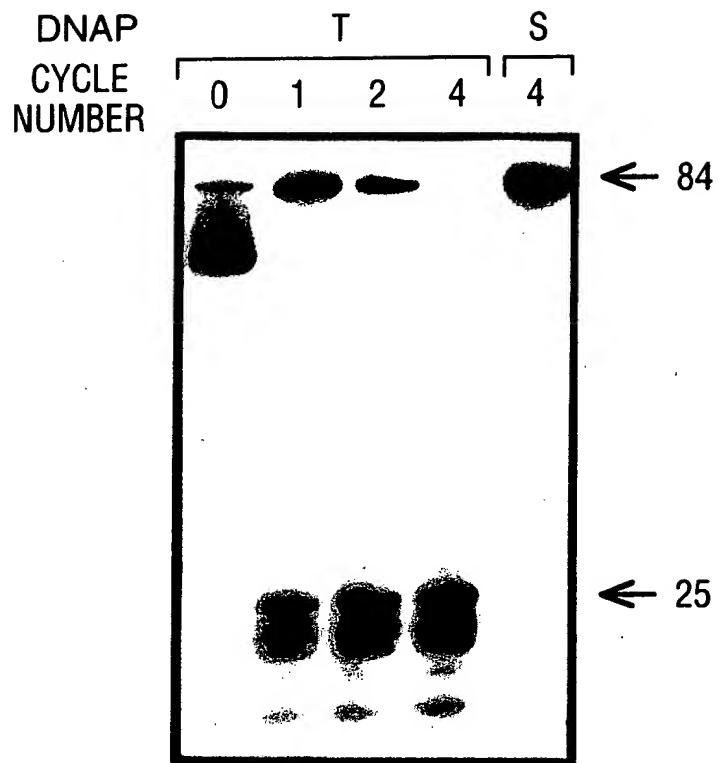


FIG. 8

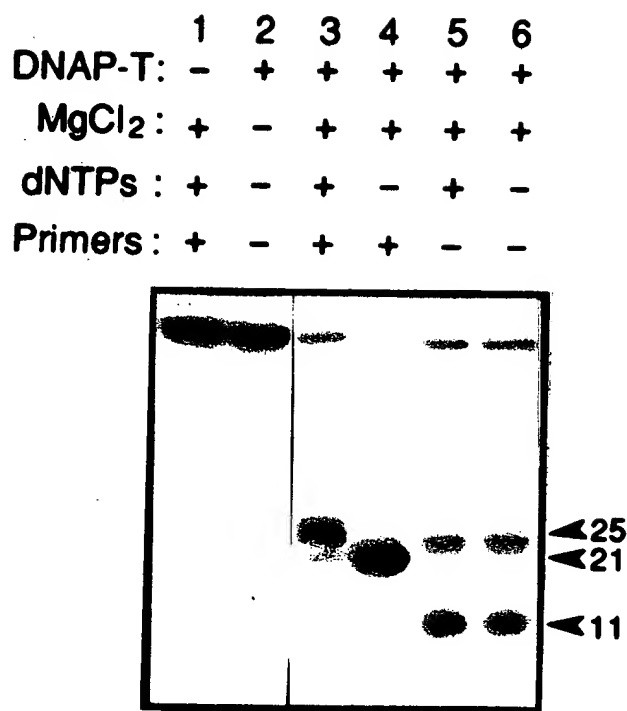


FIG. 9A

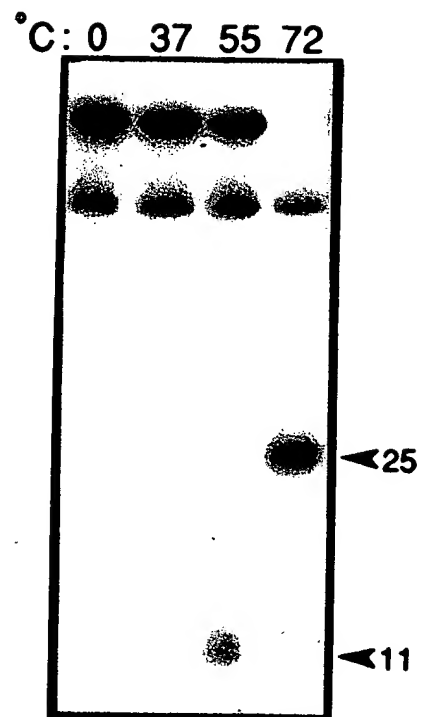


FIG. 9B

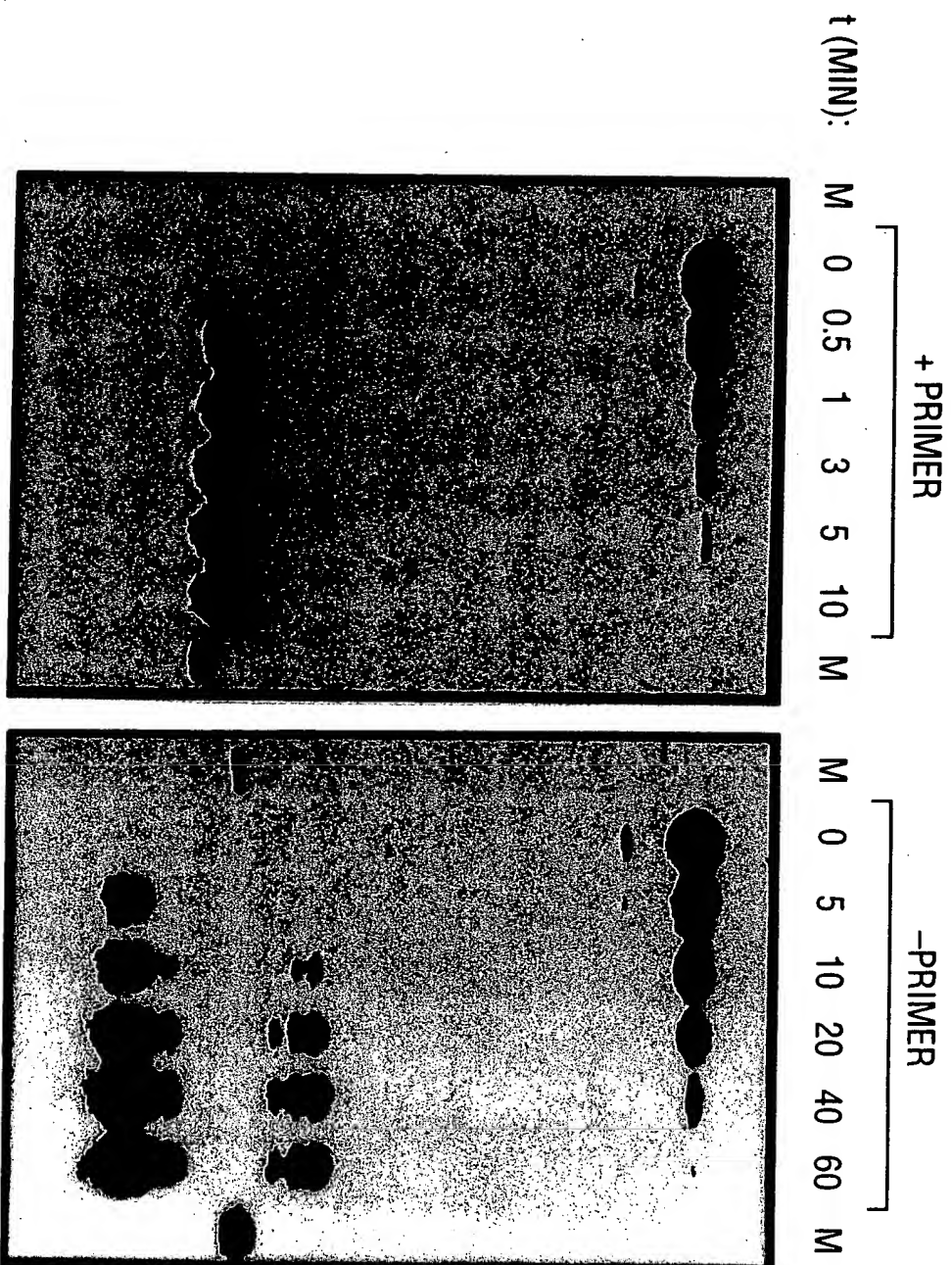


FIG. 10A

FIG. 10B



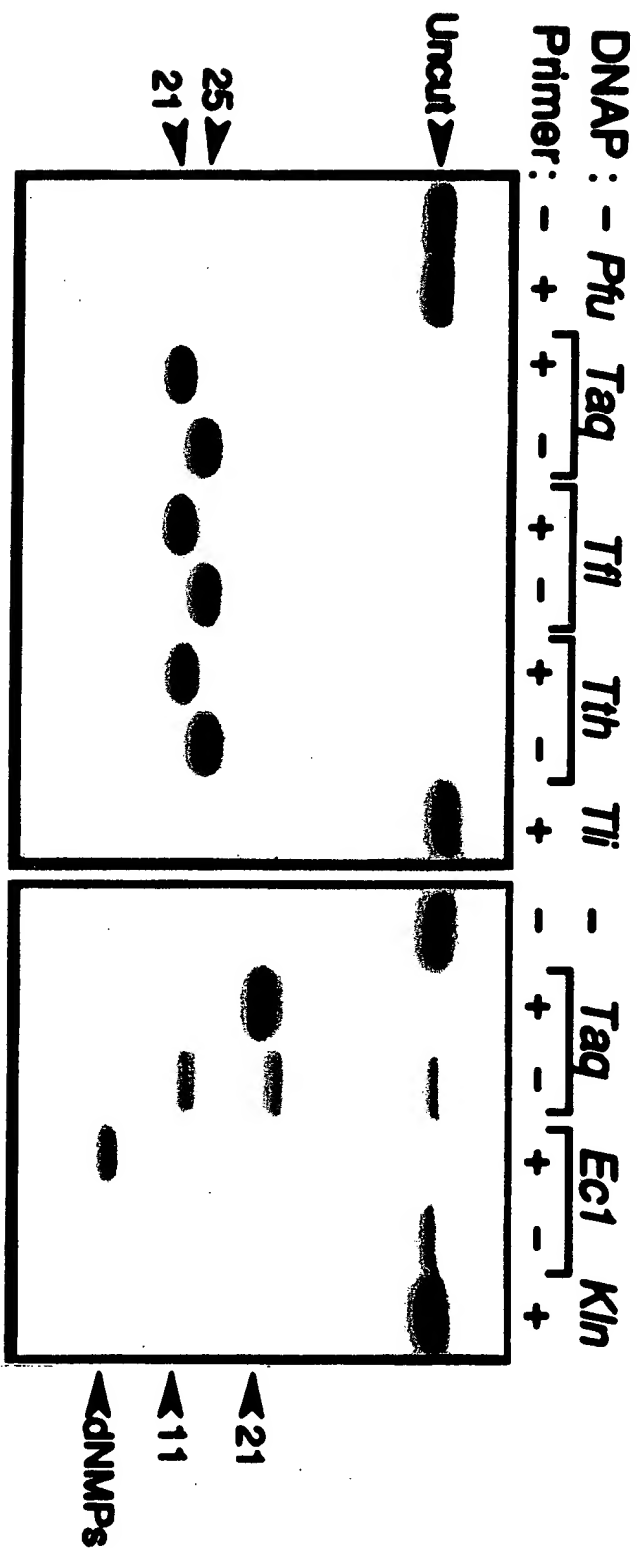
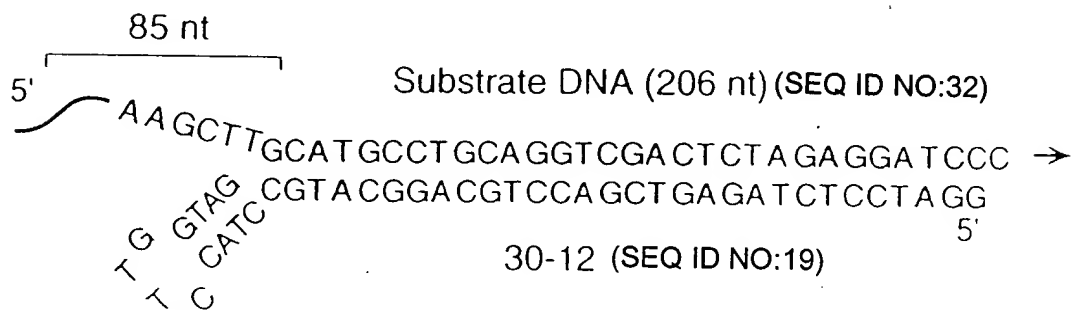
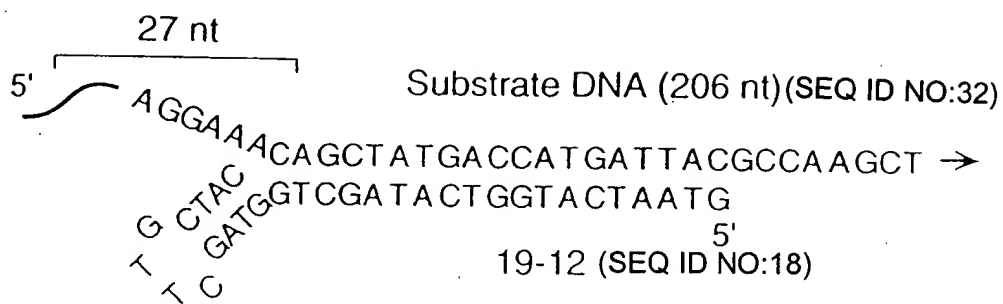
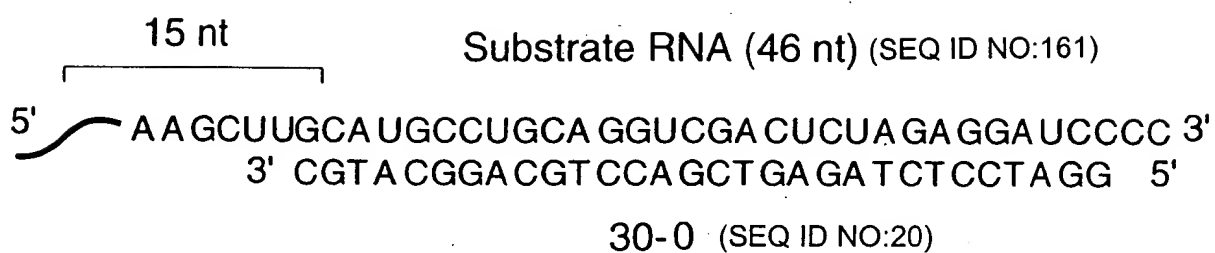


FIG. 11A

FIG. 11B

FIG. 12A





**FIG. 13A**

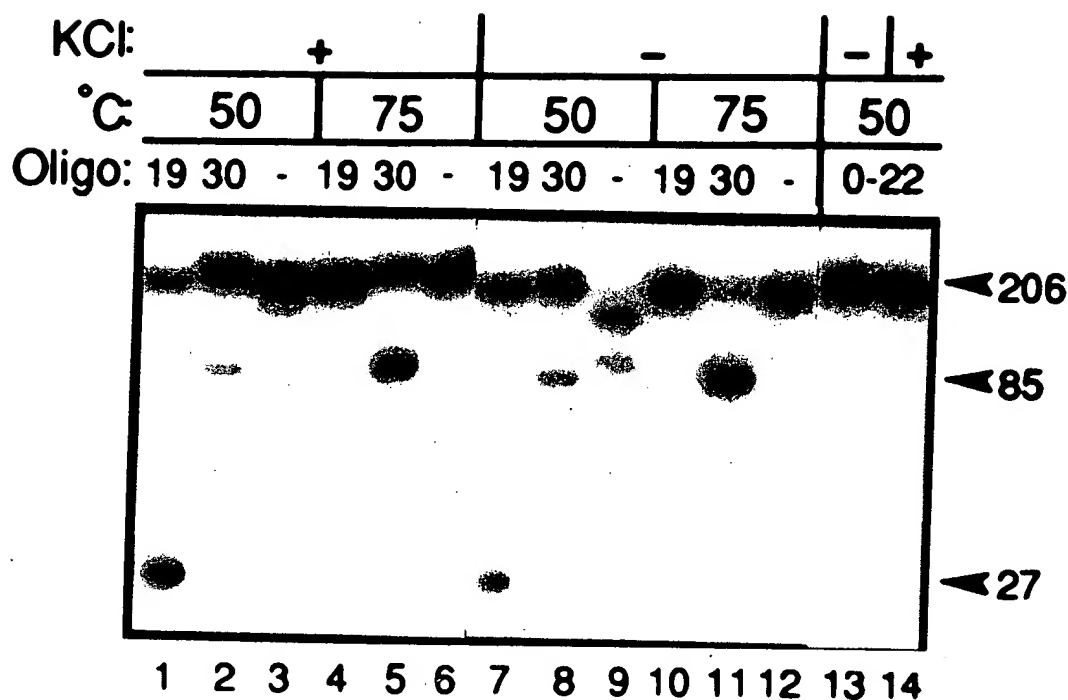


FIG. 12B

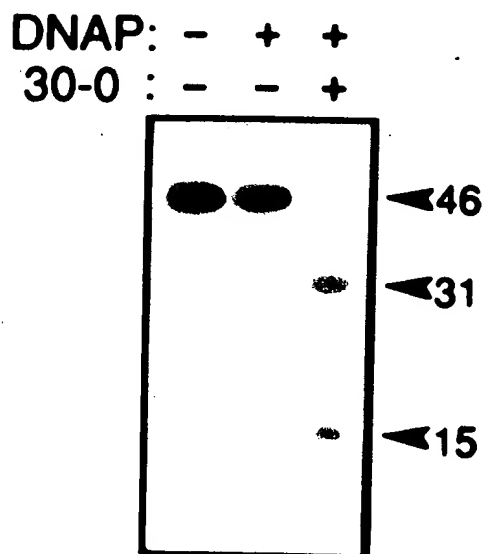
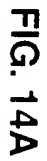
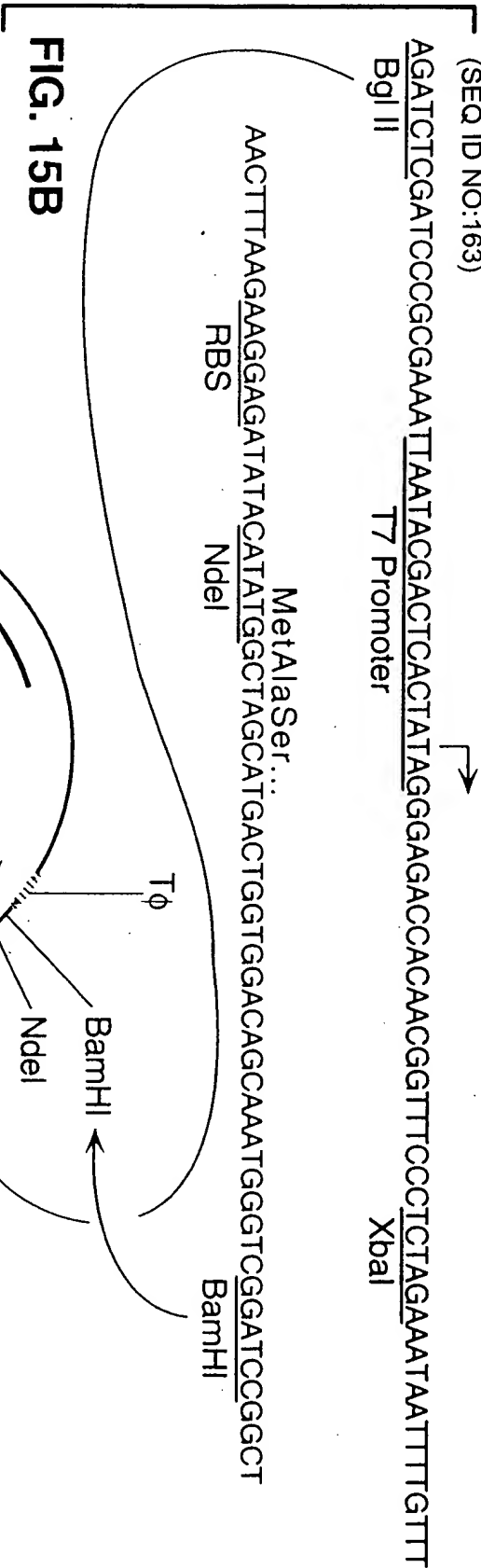


FIG. 13B

**FIG. 14B**



RBS: Ribosome binding site	lacZ: Beta-galactosidase alpha fragment
ptac: Synthetic tac promoter	rmBt: E. coli rrmB transcription terminator
lacI <sup>Q</sup> : Lac repressor gene	



Pφ10: Bacteriophage T7 φ10 promoter  
Tφ: T7 φ Terminator  
RBS: Ribosome binding site

**FIG. 15C**

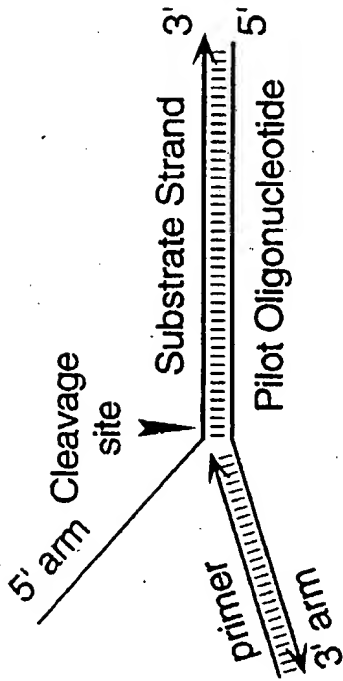


FIG. 16B

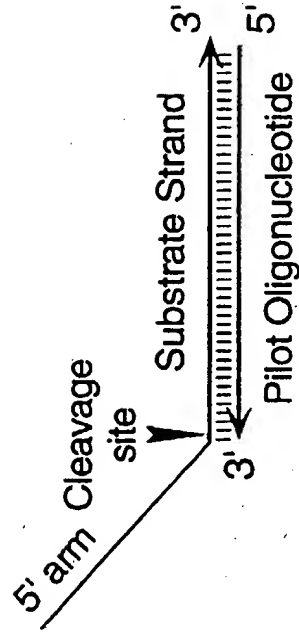


FIG. 16D

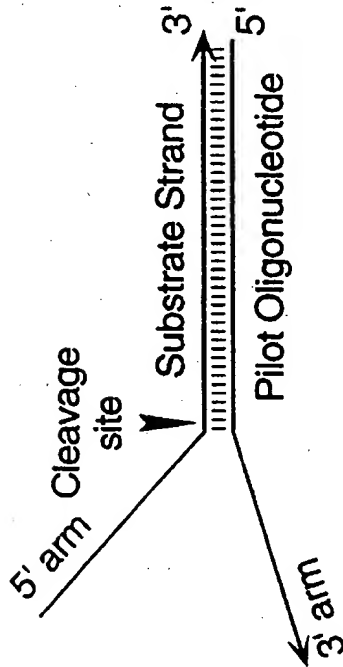


FIG. 16A

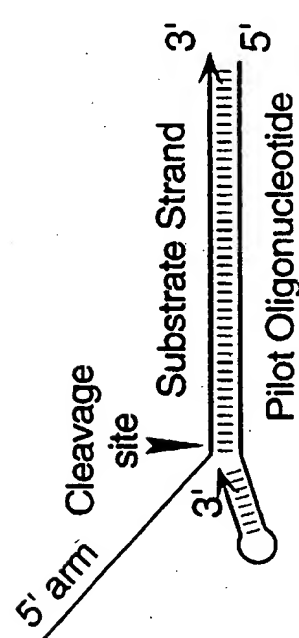


FIG. 16C

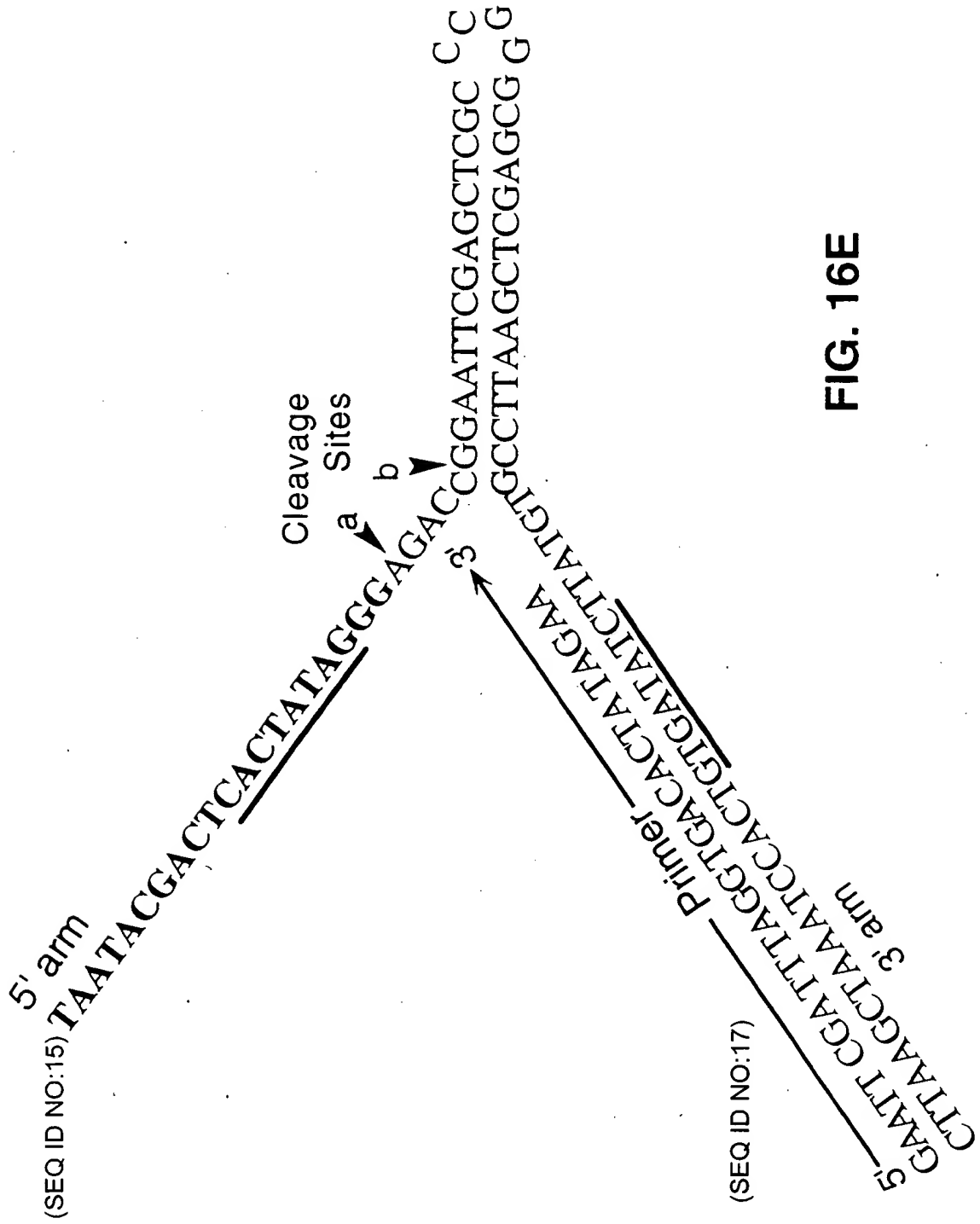


FIG. 16E



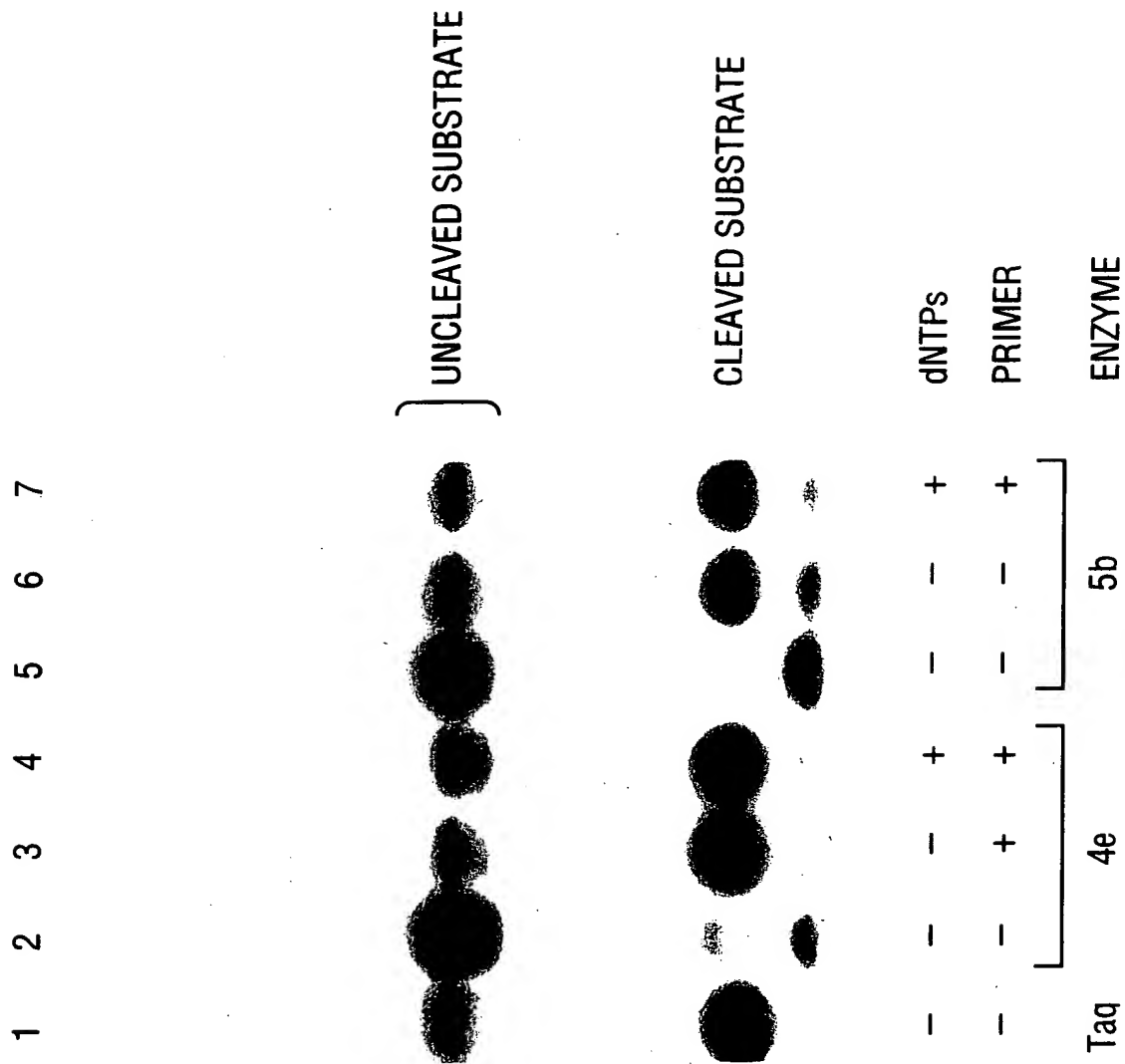


FIG. 17

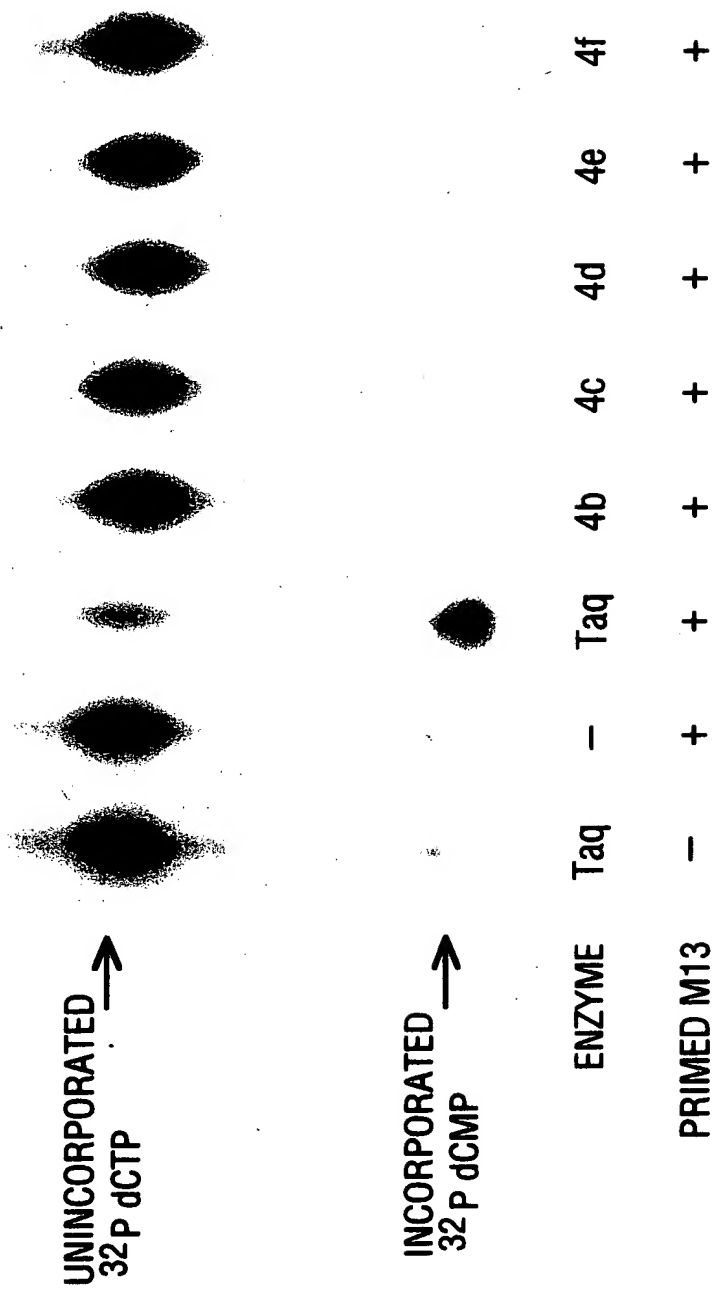
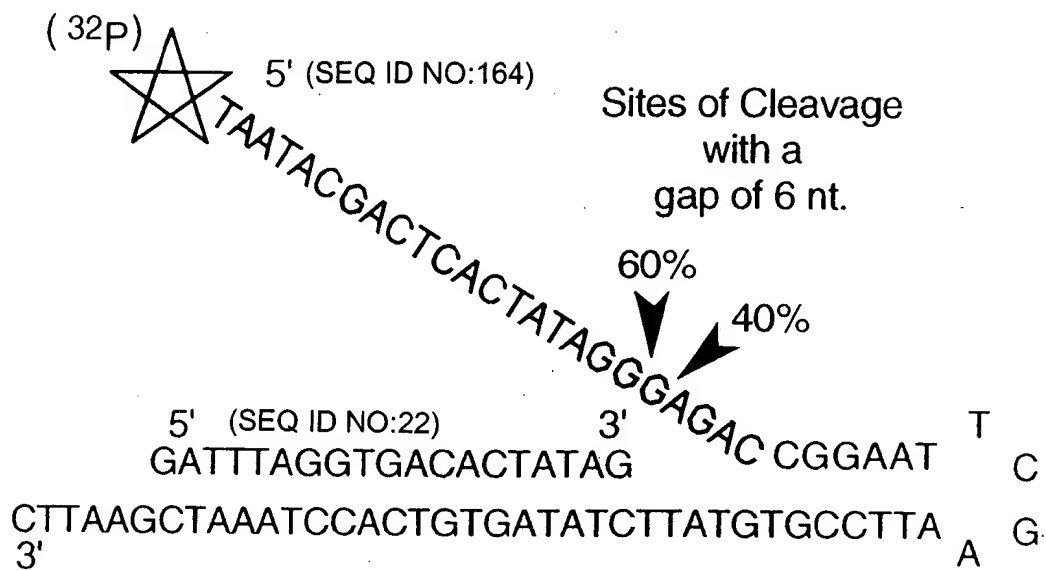


FIG. 18



**FIG. 19A**

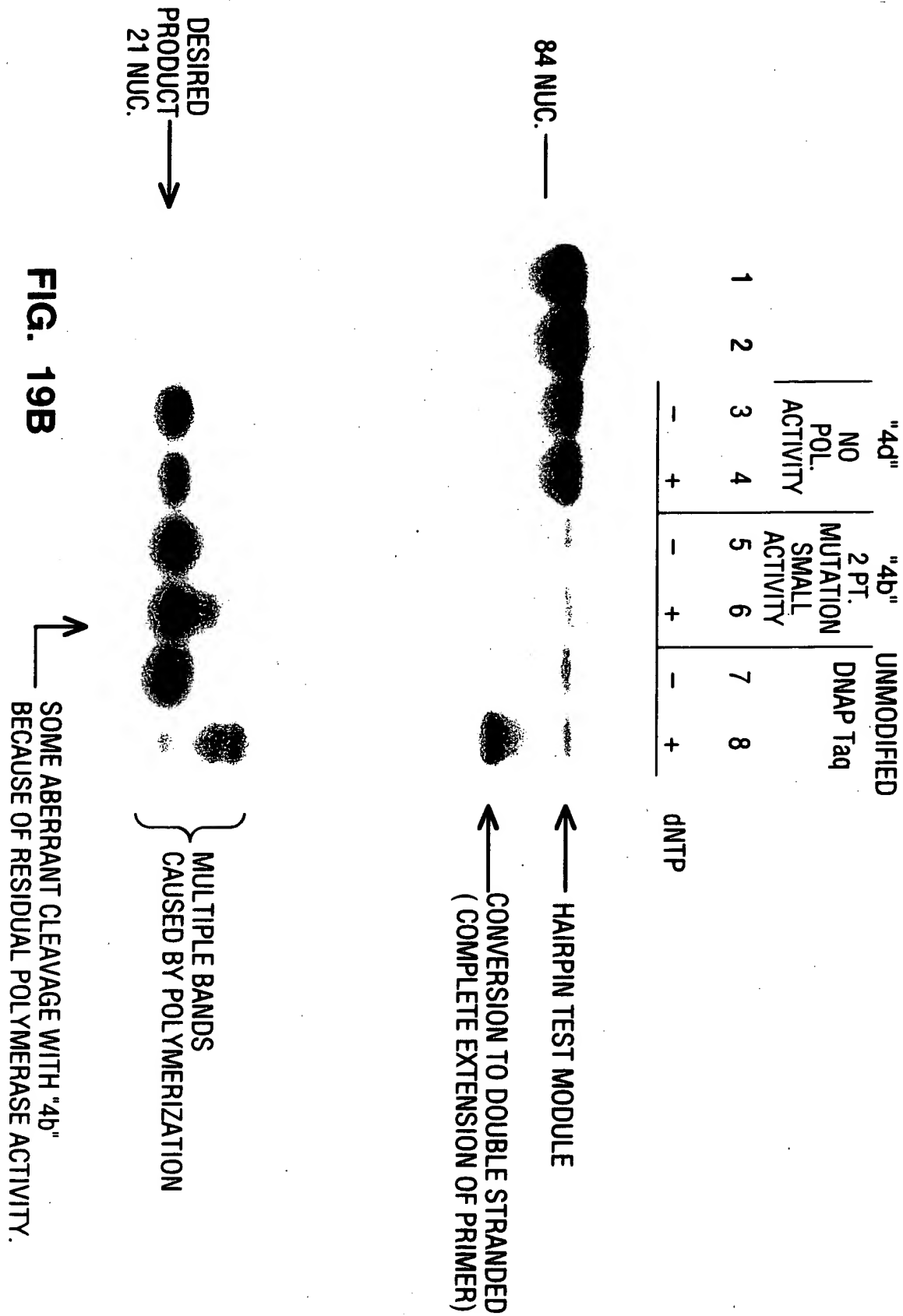


FIG. 19B

A-Hairpin  
Predicted cleavage site  
(SEQ ID NO:23)  
 $\gamma$   
5' CGACGACAAGCGAGACAGCAGCACAG GTACC A C  
3' CAAAGACGACACAGCAGGAGAGGAACGCAGAA CATGG T A

T-Hairpin  
 (SEQ ID NO:24)

Predicted  
 cleavage site

5' GTTCTGCTGTCGTCCTCTCTGCTCTT  
     5' Alpha primer 3' GTACCATGG A T  
 3' CTGCTTGTCGCTCTCTGCTGTC T G

## FIG. 20A

Sequence of alpha primer: (SEQ ID NO:25)  
5' GACGAACAAGCGAGACAGCG 3'

**FIG. 20B**

5' ACACAG GTACC A C  
3' CAAAGACGACACAGCAGAGAGAGAA CATGG T A

5' Tau primer 3'

FIG. 20C Cleaved A-Hairpin

5' ACACAG GTACC A C  
 3' CATGG T A  
 GGAGACGGAGAA  
 Cleaved A-Hairpin  
 (SEQ ID NO:28)  
 NlaIII HgiCI  
 5' CCTCTT GTACC A T  
 3' CTGCTGTTCGCTCTGCGCTGTC  
 Alpha primer 3'  
 Cleaved T-Hairpin  
 (SEQ ID NO:27)

## FIG. 20C

(SEQ ID NO:26) (SEQ ID NO:27)  
 5' GTTCTGCTGTGTCGTCCTCTCTTGCCTCTTGATACCATGGTACCTGTGCGCTGCTGCTTGGTC  
 3' CAAAGACGACACAGCAGAGAGAAACGAGAACATGGTACACCATGGACACAGGACAGAGCGAAACGAGGC 5'  
 FIG. 20D  
 (SEQ ID NO:23)

**FIG. 20D**

A-Hairpin  
(SEQ ID NO:23)

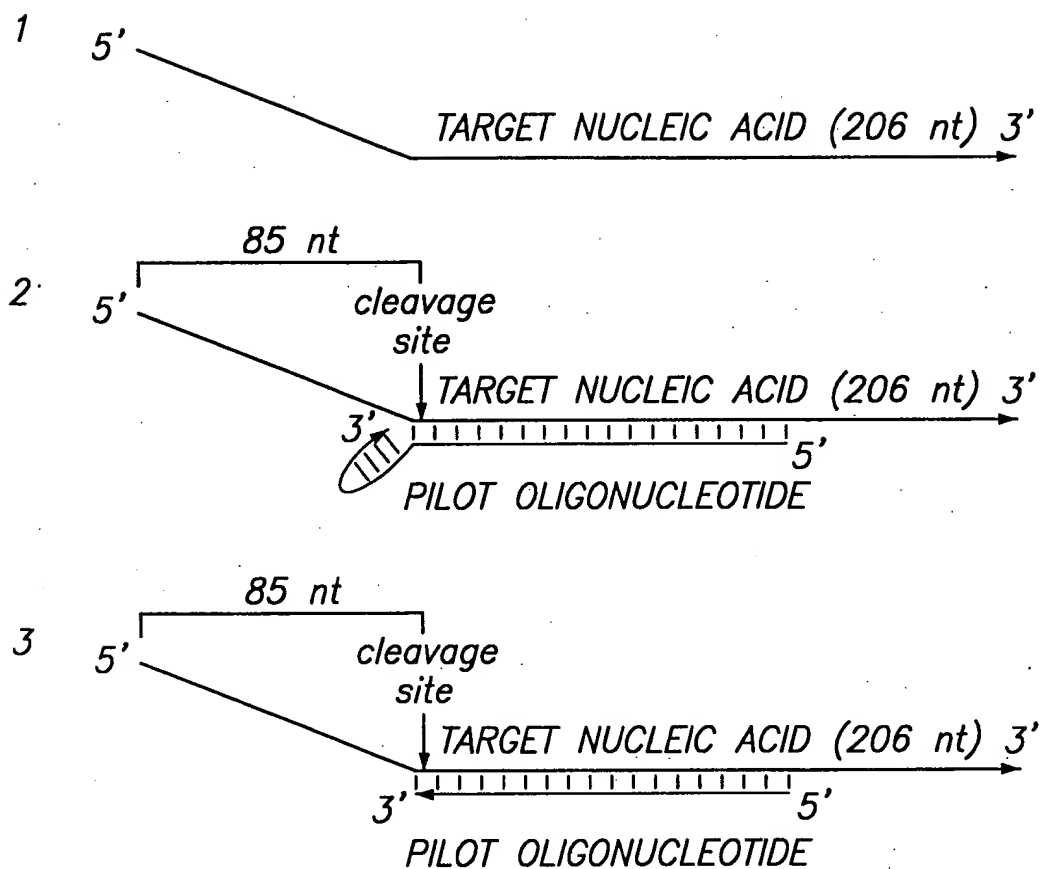
ECOR. 1

FM 101-30-0

↑ 57

206

**FIG. 21**



**FIG. 22A**

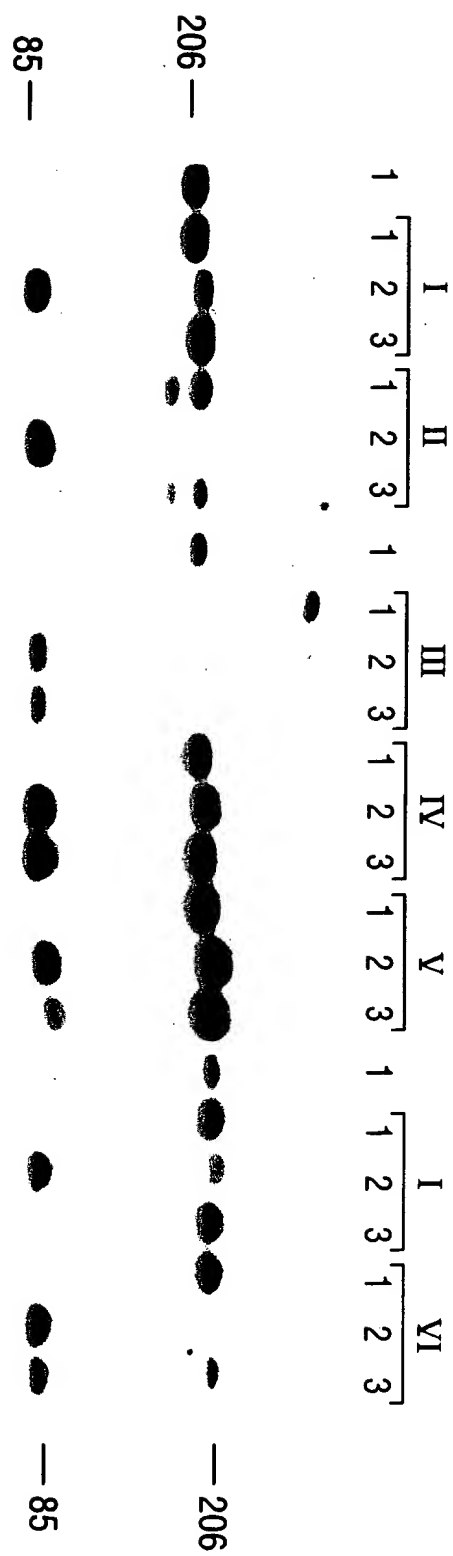


FIG. 22B



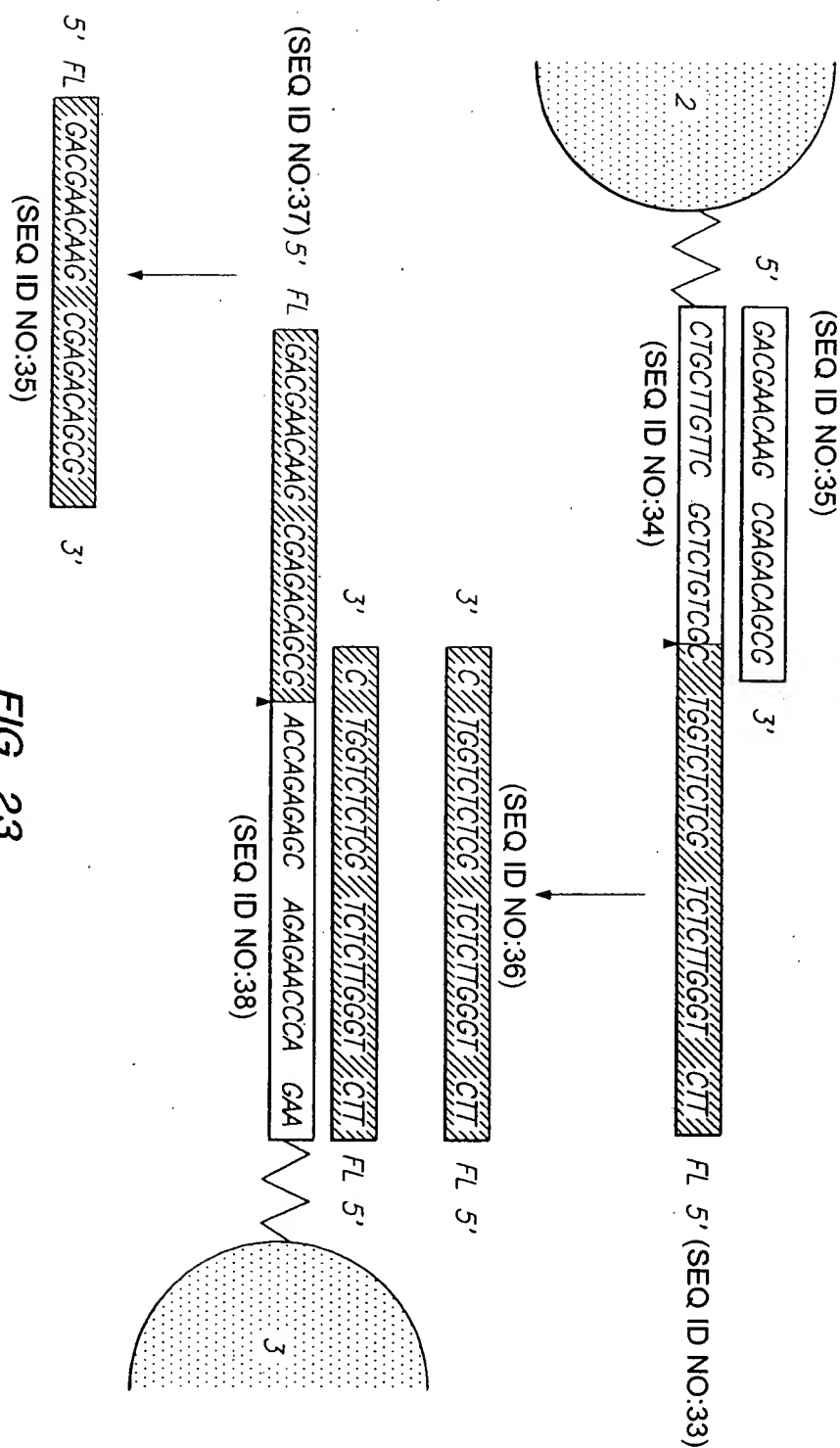


FIG. 23

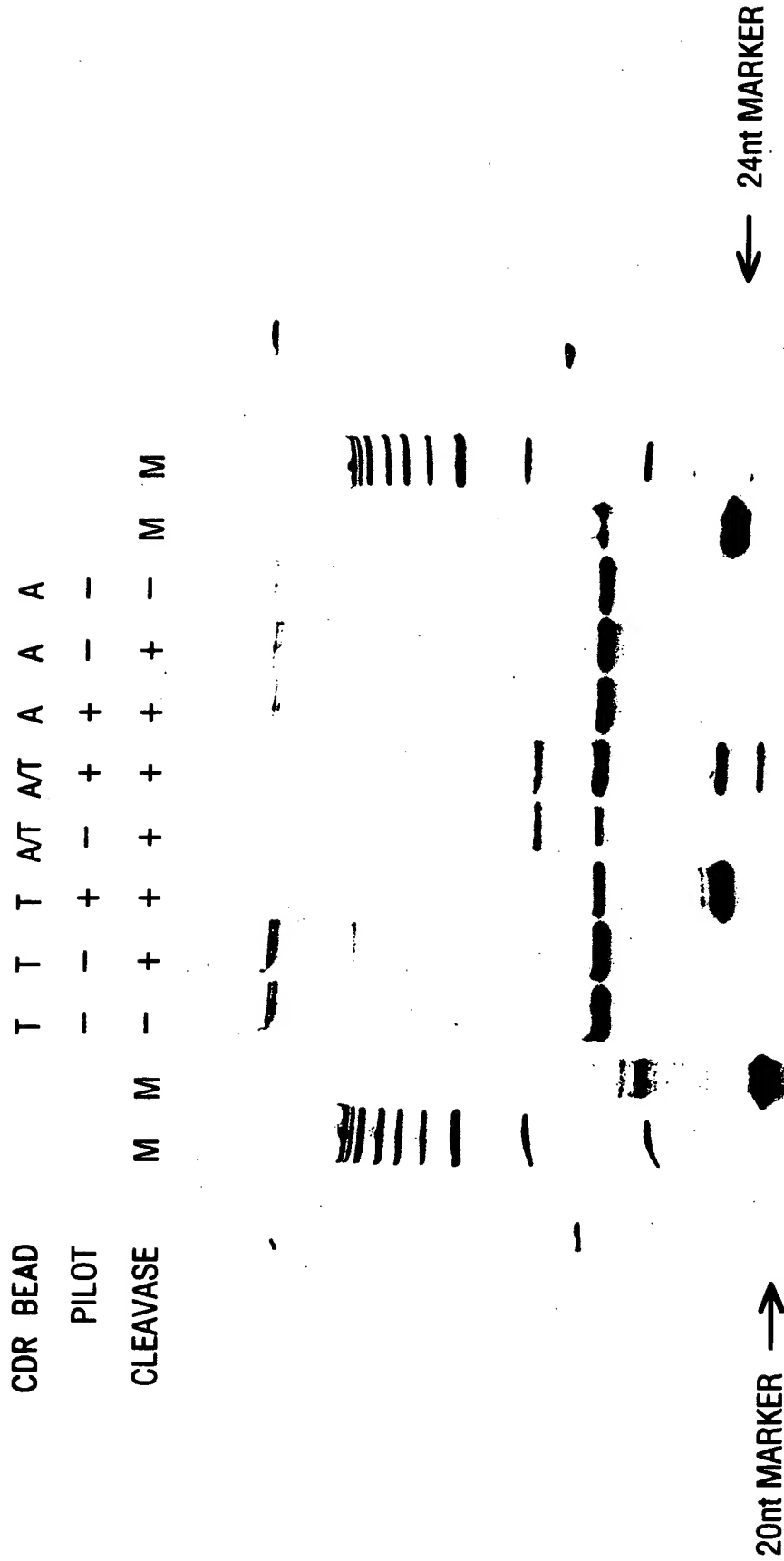


FIG. 24

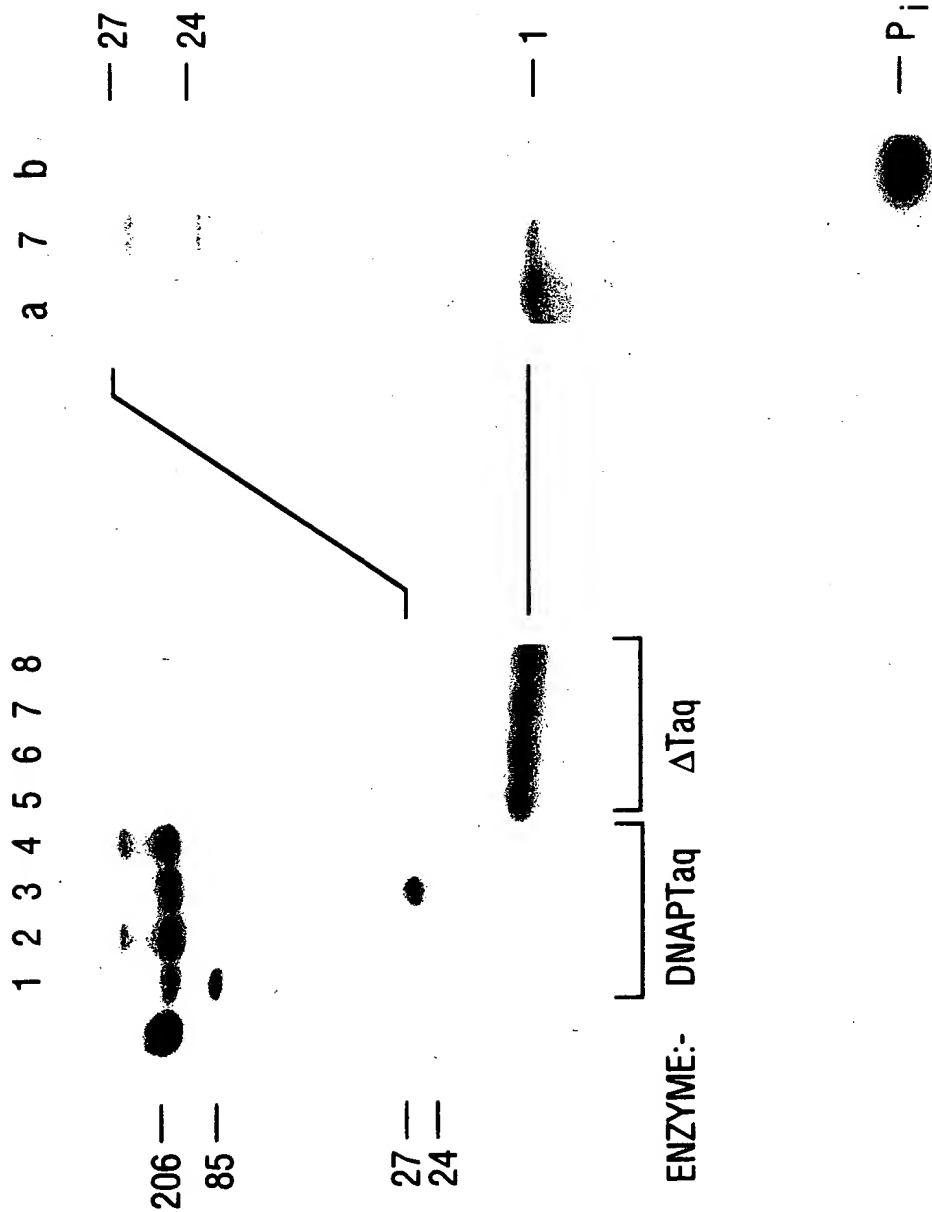


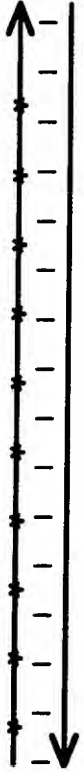
FIG. 25A

FIG. 25B

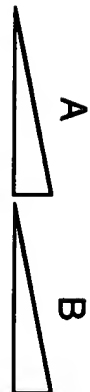
**FIG. 26A**



**FIG. 26B**



\* = 32p



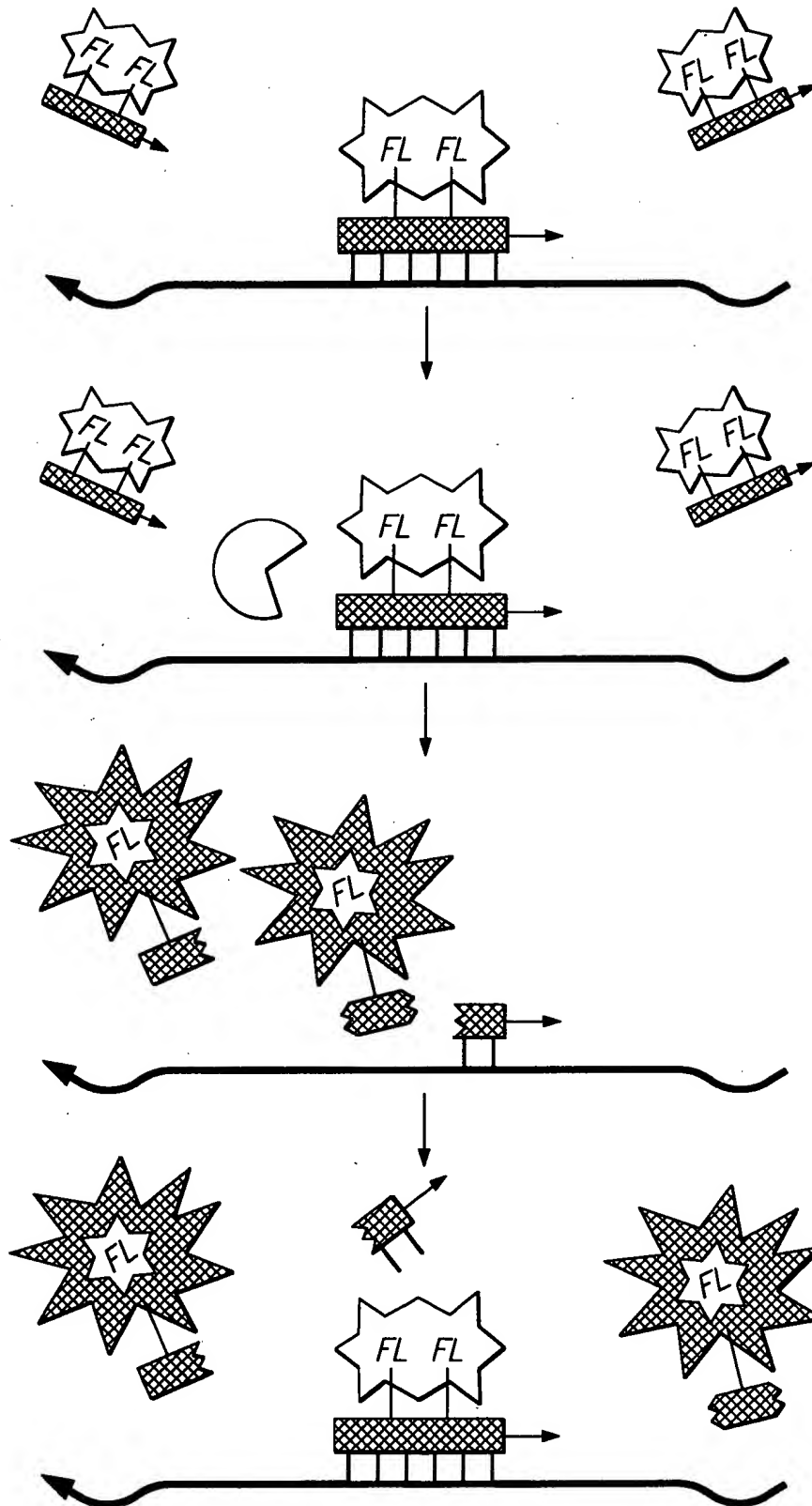
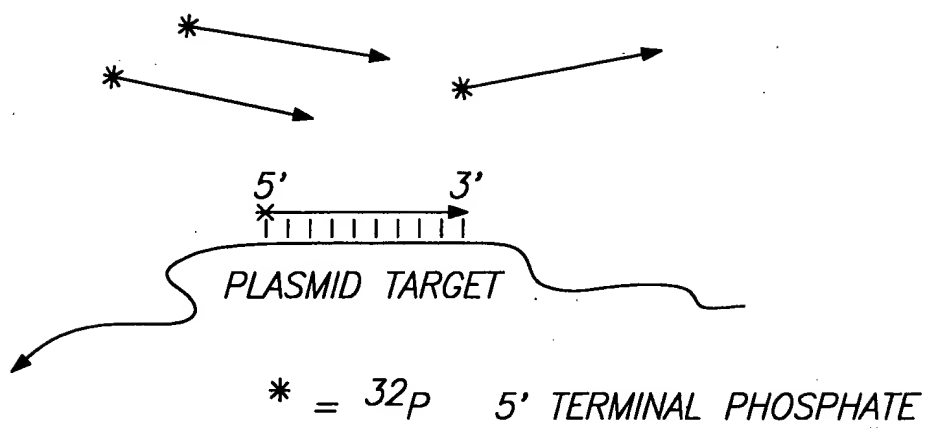
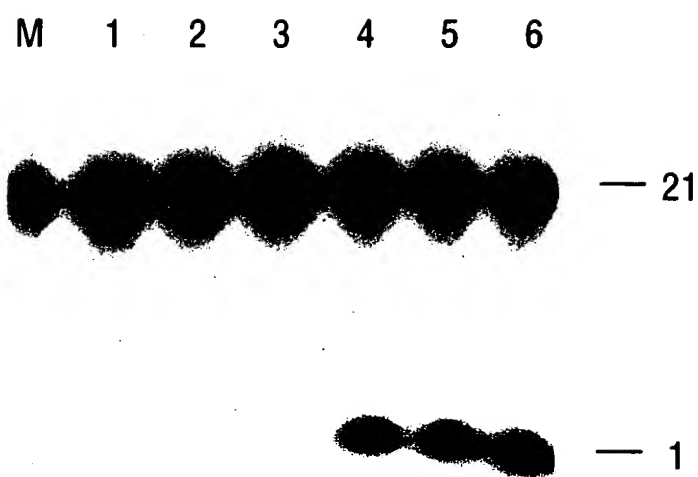


FIG. 27



**FIG. 28A**



**FIG. 28B**

Wild-Type Substrate

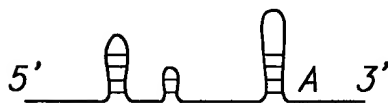
Mutant Substrate



1  
Denature



2  
Renature



3  
Add cleavage agent



▴ = cleavage site

4  
Resolve reaction products

5  
Detect unique cleavage "fingerprint"

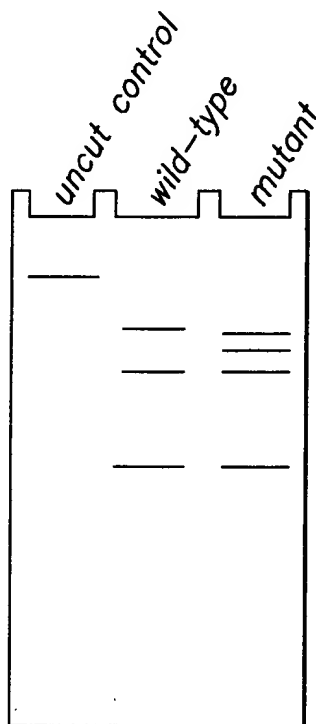
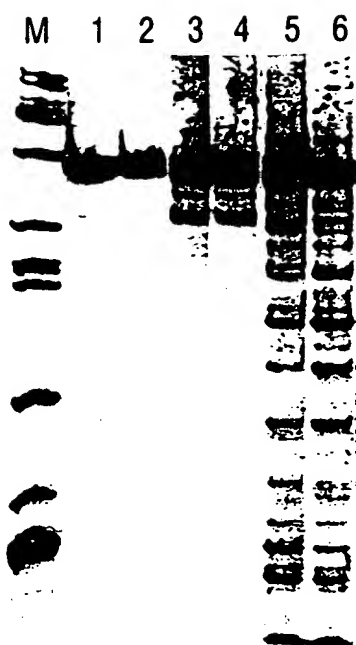


FIG. 29





**FIG. 30**

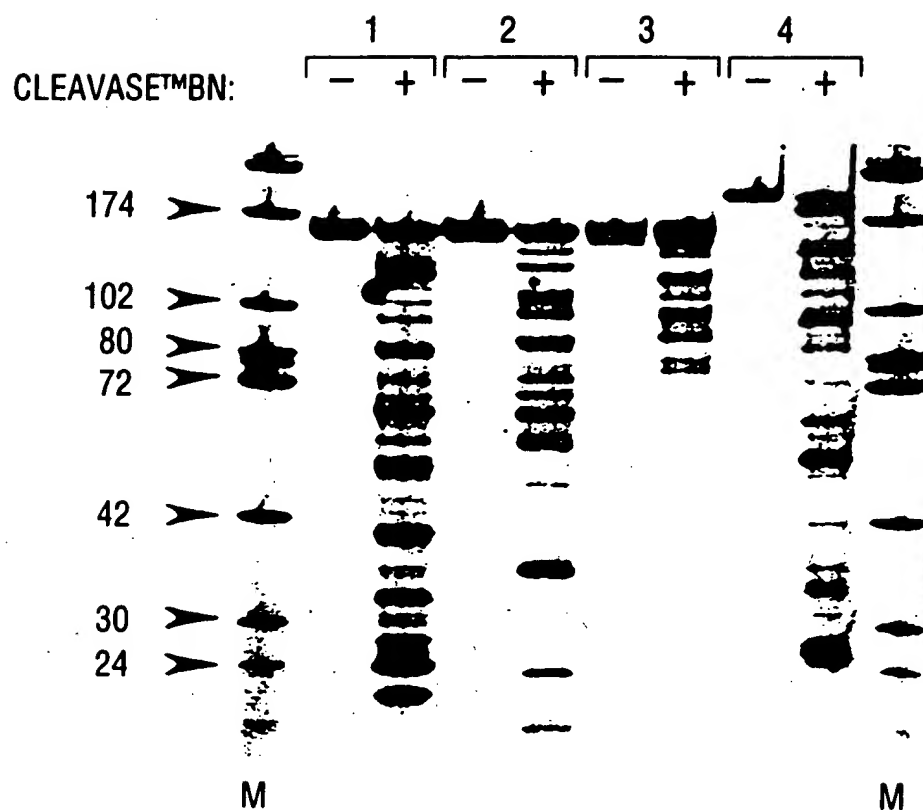


FIG. 31

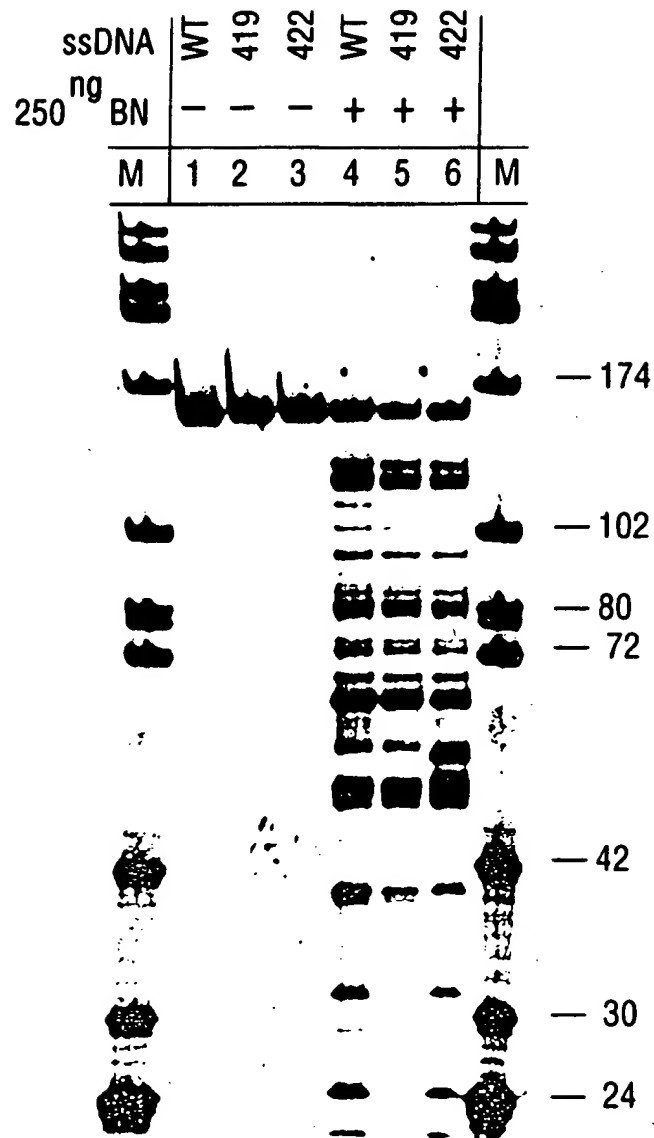


FIG. 32

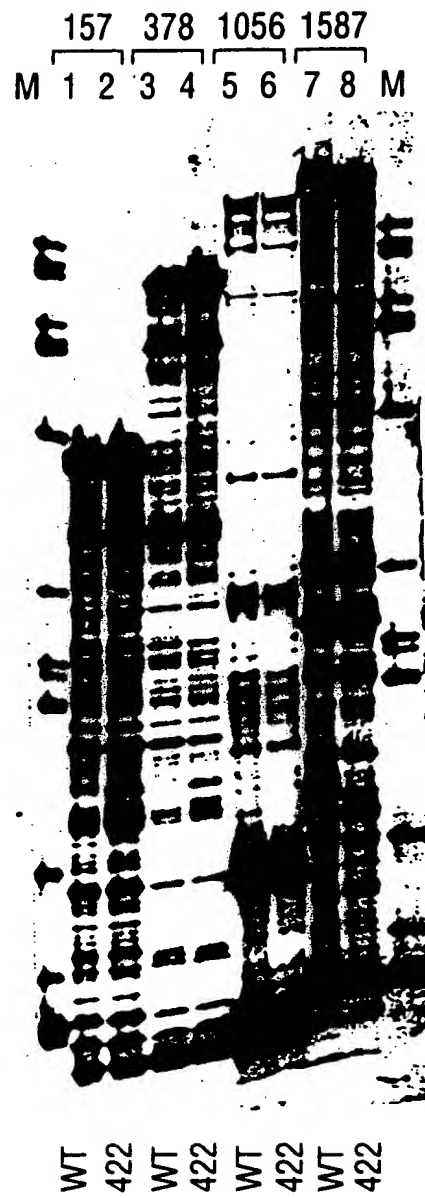
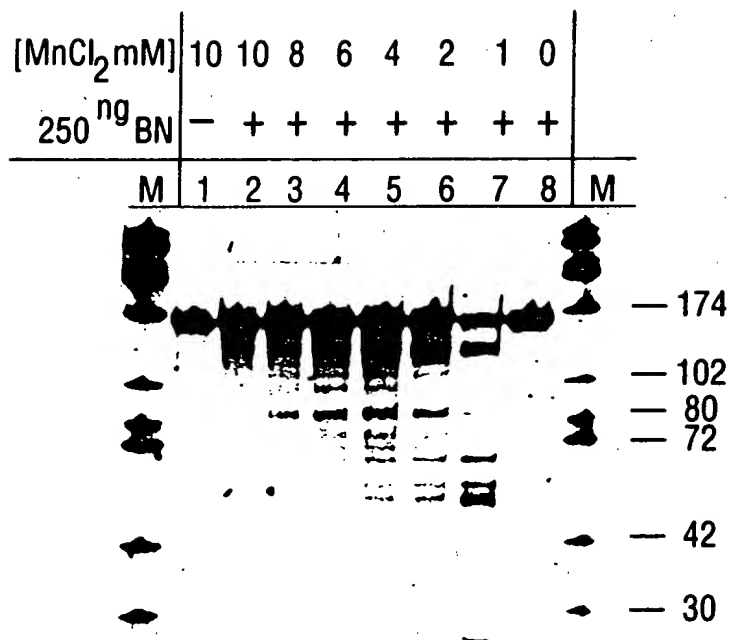


FIG. 33



**FIG. 34**

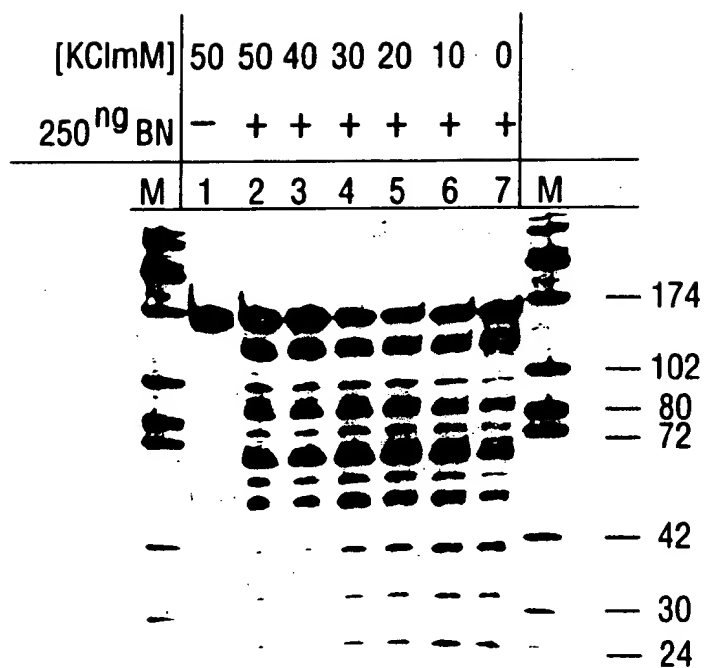


FIG. 35

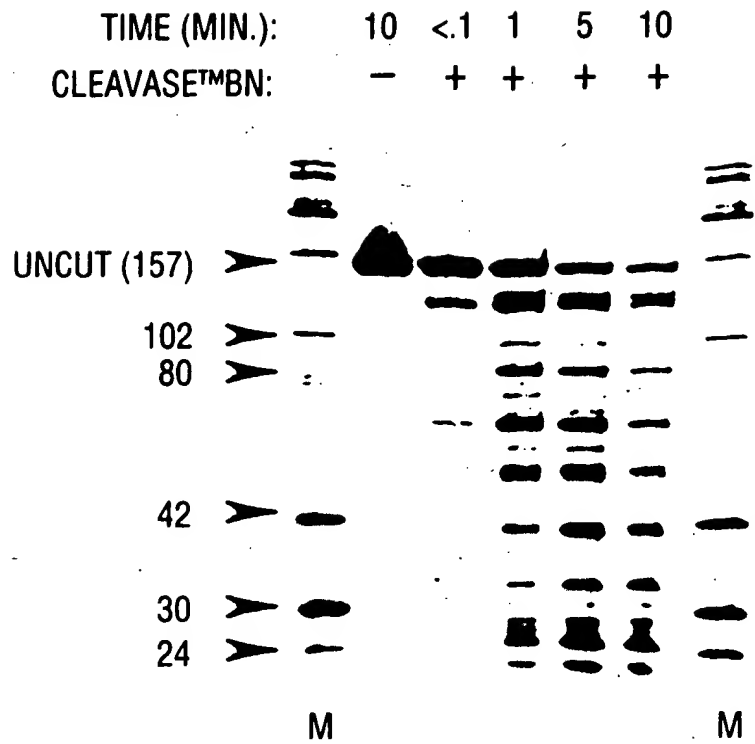


FIG. 36





CLEAVASE™BN (ng):      — 10 50 100 250



FIG. 38

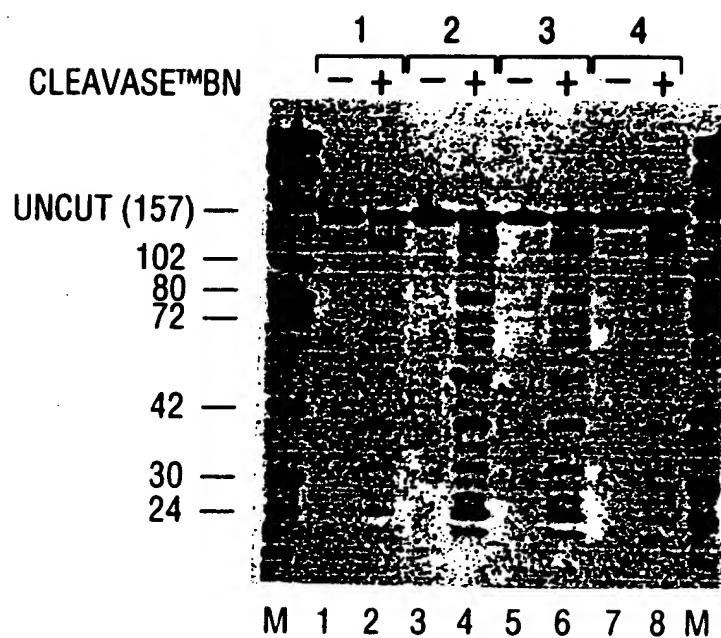


FIG. 39

STRAND	5' - BIOTIN SENSE STRAND						5' - FLUORESCIN ANTI-SENSE STRAND					
ssDNA	WT	419	422	WT	419	422	WT	419	422	WT	419	422
250 <sup>ng</sup> BN	-	-	-	+	+	+	+	+	+	-	-	-
M	1	2	3	4	5	6	7	8	9	10	11	12

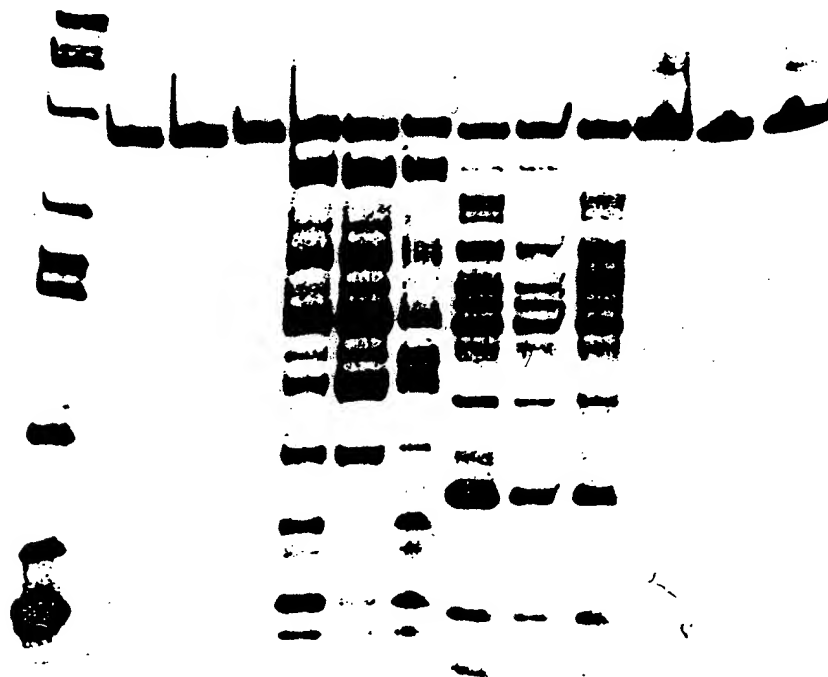


FIG. 40

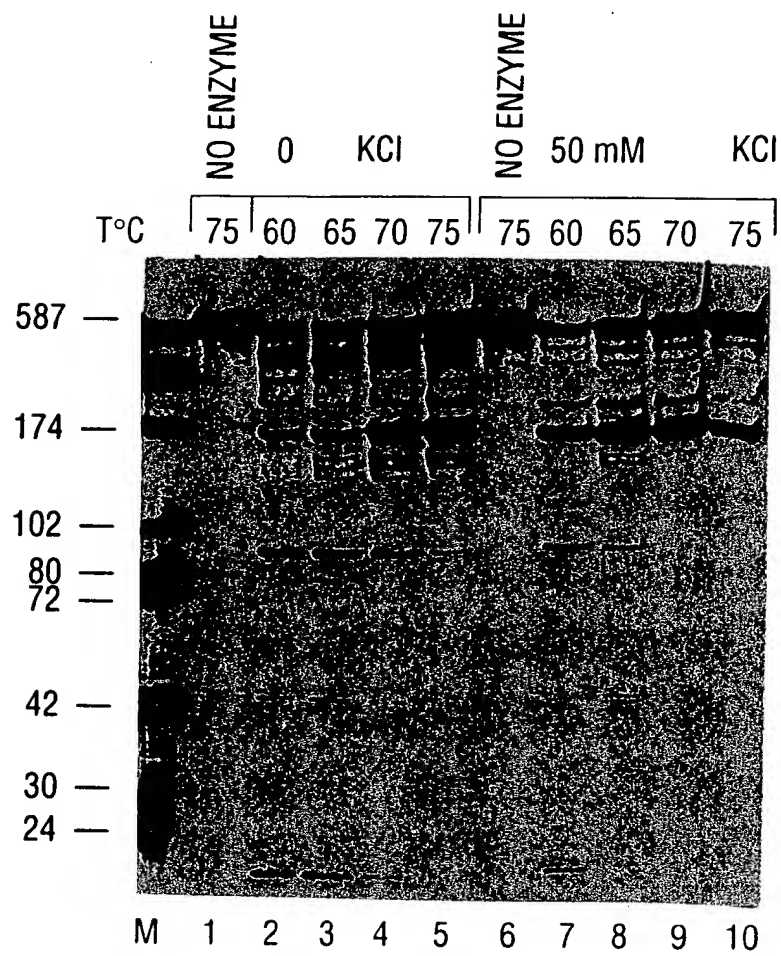


FIG. 41

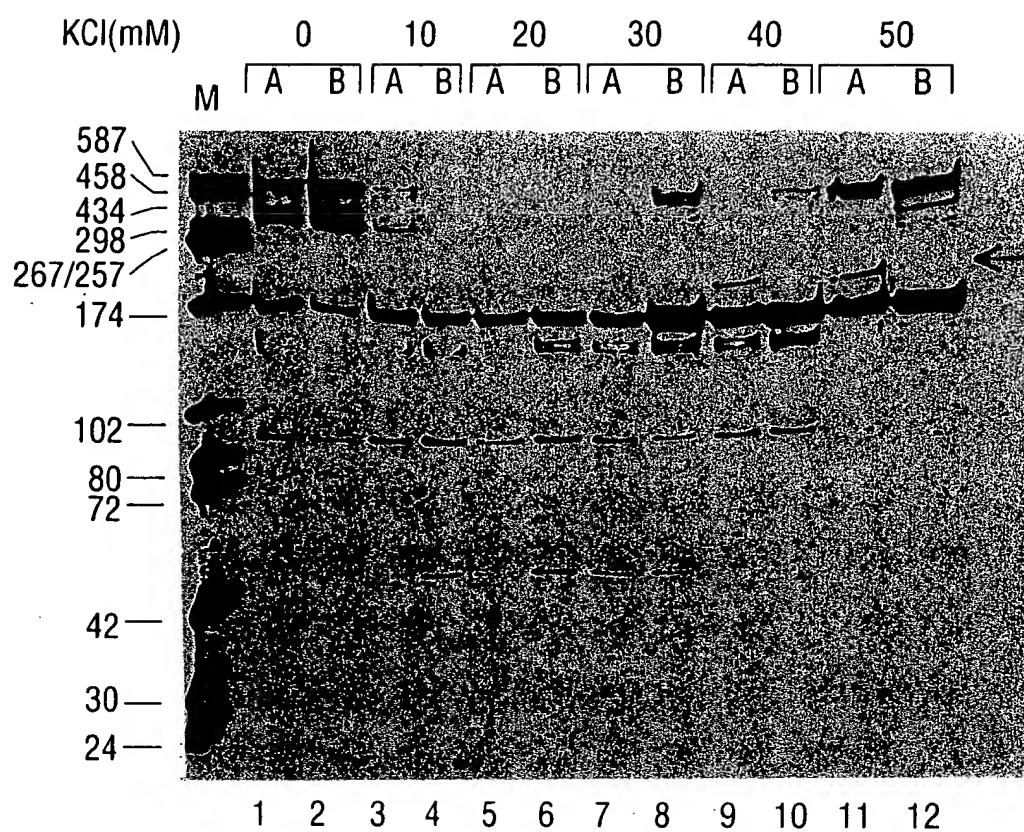


FIG. 42

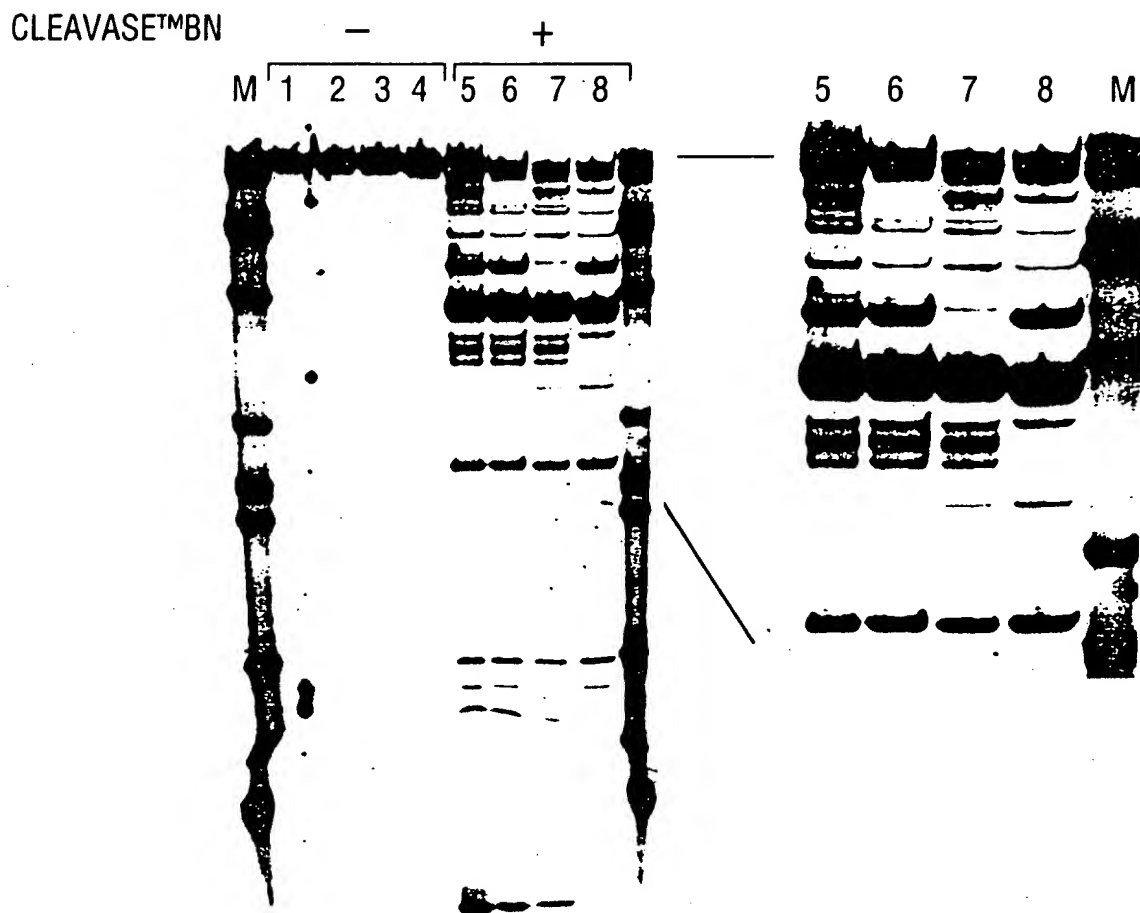


FIG. 43

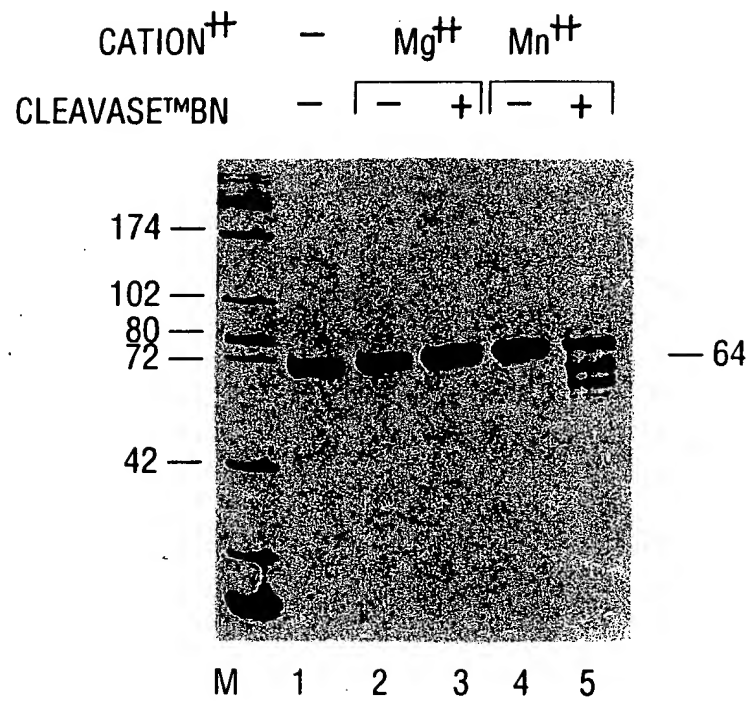


FIG. 44

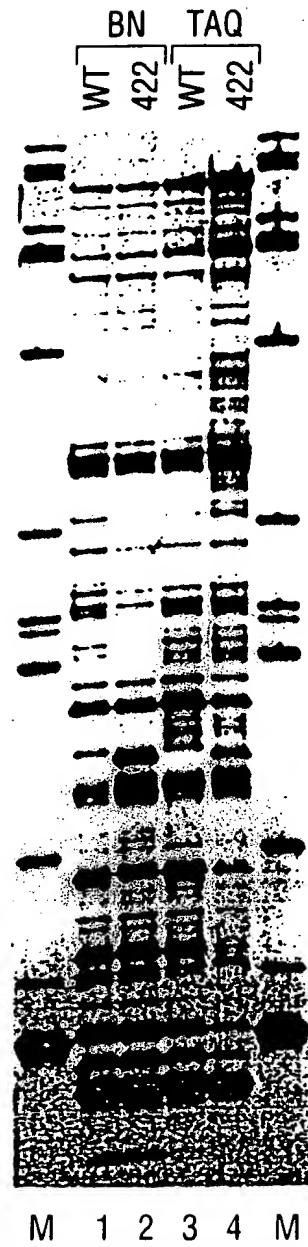


FIG. 45



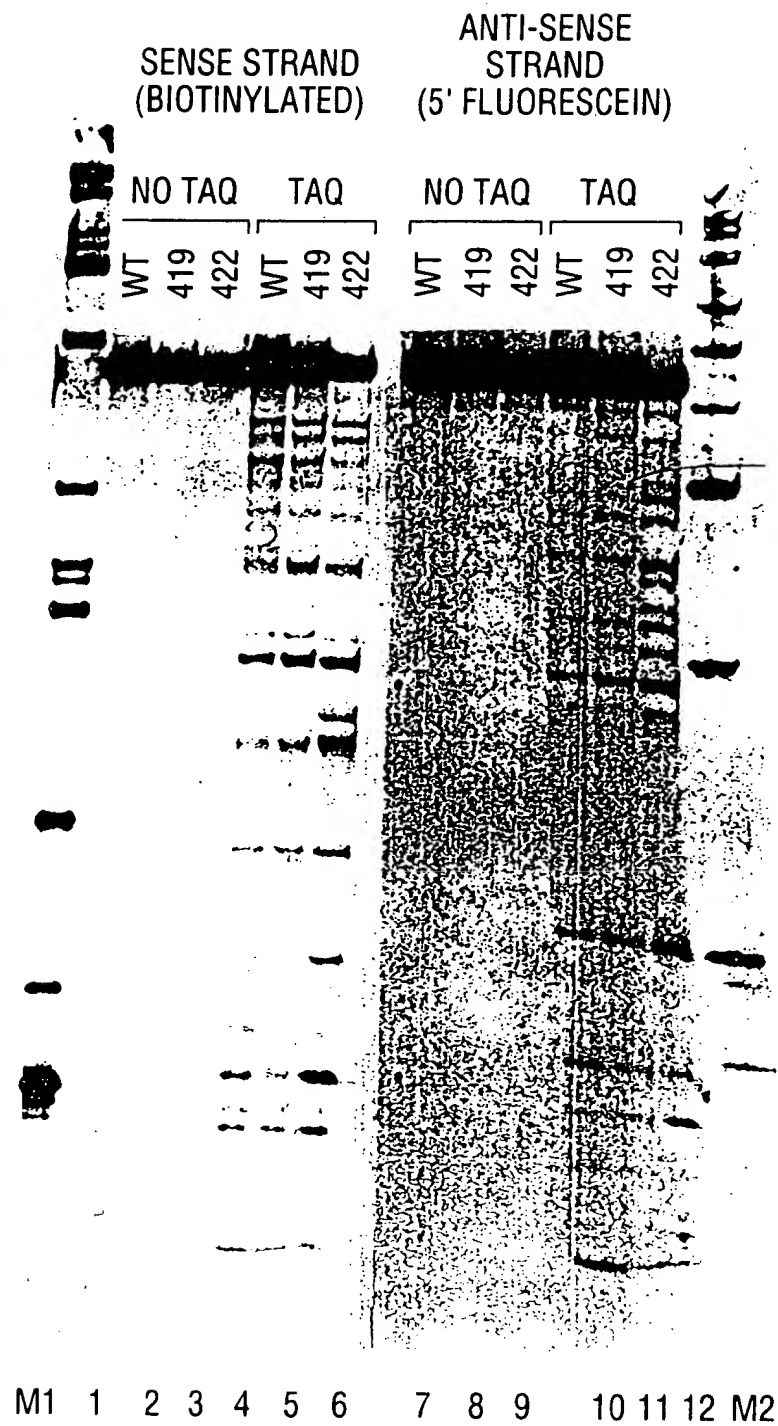
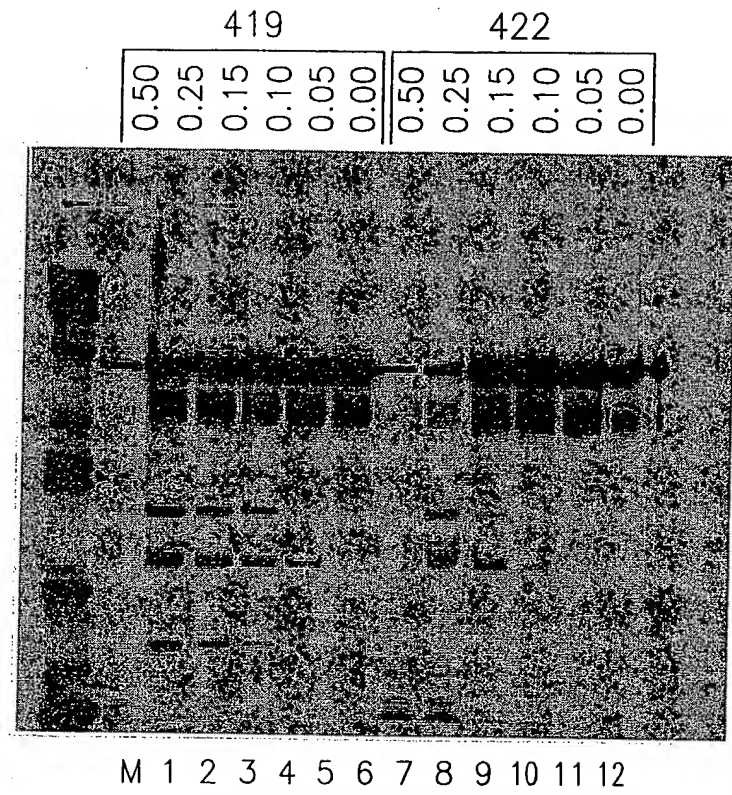


FIG. 46



**FIG. 47**

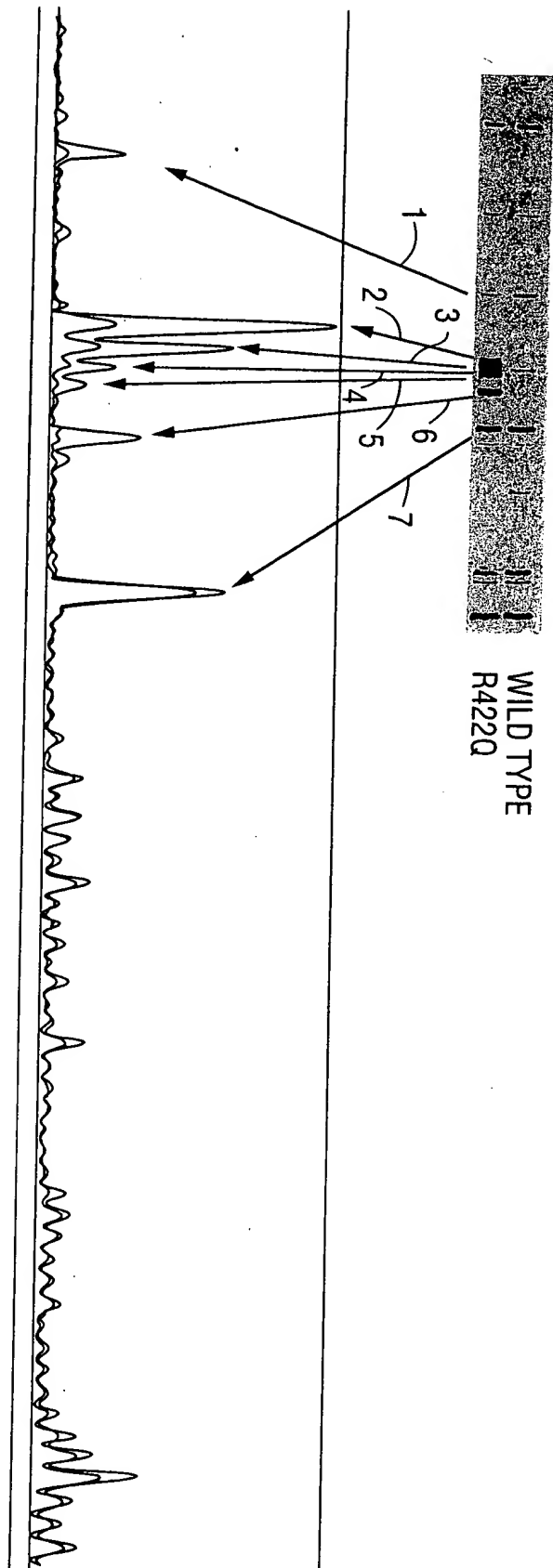


FIG. 48

50

L.100.8-1            5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG  
(SEQ ID NO: 76) 3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCTCCCTGAAAGGTGTTCCCC

L.46.16-10           5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG  
(SEQ ID NO: 77) 3'CCGACTGTTCTTCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L.46.16-12           5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG  
(SEQ ID NO: 78) 3'CCGACTGTTCTTCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L19.16-3            5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG  
(SEQ ID NO: 79) 3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCTCCCTGAAAGGTGTTCCCC

L.CEM/251           5'GGCTGACAAGAAGGAAACTCGCTGAAACAGCAGGGACTTTCCACAAGGGG  
(SEQ ID NO: 80) 3'CCGACTGTTCTTCCTTTGAGCGACTTTGTCTCCCTGAAAGGTGTTCCCC

L.36.8-3            5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG  
(SEQ ID NO: 81) 3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCTCCCTGAAAGGTGTTCCCC

**FIG. 49A**

L.100.8-1	100	ATGTTACGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT
(SEQ ID NO: 76)		TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGTGAGAGA
L.46.16-10		ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTCT
(SEQ ID NO: 77)		TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGGTGAAAGA
L.46.16-12		ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTCT
(SEQ ID NO: 78)		TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGGTGAAAGA
L19.16-3		ATGTTACGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCTCTCT
(SEQ ID NO: 19)		TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGGAGAGA
L.CEM/251		ATGTTACGGGAGGTACTGGGAAGGAGCCGGTCGGGAACGCCCACTTTCT
(SEQ ID NO: 80)		TACAATGCCCCCTCCATGACCCCTTCTCGGCCAGCCCTTGCGGTGAAAGA
L.36.8-3		ATGTTACGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT
(SEQ ID NO: 81)		TACAATGCCCTCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGTGAGAGA

**FIG. 49B**

L. 100.8-1	<div>150</div> 5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACTACATATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT
L. 46.16-10	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACTACATATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT
L. 46.16-12	5'TGGTGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACCACATATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT
L. 19.16-3	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACTACATATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT
L. CEM/251	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACTACATATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT
L. 36.8-3	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACTACATATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT

**FIG. 49C**

L.100.8-1	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	200
L.46.16-10	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.46.16-12	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.19.16-3	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.CEM/251	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.36.8-3	GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGATCCTCCAAGAGAGGTCGTGATCGTCCATC	

**FIG. 49D**

L. 100. 8 -1	5'AGCCTGGGTGTTCCCTGCTAGAC	TCTCACCAGCAC	TTGGCCGGTGCTGGG
(SEQ ID NO: 76)	3'TCGGACCCACAAAGGACCATCTG	AGAGTGGTCGTGAAC	CGCCACGACCC
L. 46.16-10	5'AGCCTGGGTGTTCCCTGCTAGAC	TCTCACCAGCAC	TTAGCCAGTGCTGGG
(SEQ ID NO: 77)	3'TCGGACCCACAAAGGACGATCTG	AGAGTGGTCGTGAAT	CGGTCACGACCC
L. 46.16-12	5'AGCCTGGGTGTTCCCTGCTAGAC	TCTCACCAGCAC	TTGGCCAGTGCTGGG
(SEQ ID NO: 78)	3'TCGGACCCACAAAGGACGATCTG	AGAGTGGTCGTGAAC	CGGTCACGACCC
L. 19.16-3	5'AGCCTGGGTGTTCCCTGCTAGAC	TCTCACCAGCAC	TTGGCCGGTGCTGGG
(SEQ ID NO: 79)	3'TCGGACCCACAAAGGACGATCTG	AGAGTGGTCGTGAAC	CGCCACGACCC
L. CEM/251	5'AGCCTGGGTGTTCCCTGCTAGAC	TCTCACCAGCAC	TTGGCCGGTGCTGGG
(SEQ ID NO: 80)	3'TCGGACCCACAAAGGACGATCTG	AGAGTGGTCGTGAAC	CGCCACGACCC
L. 36.8-3	5'AGCCTGAGTGTTCCCTGCTAAAC	TCTCACCAGCAC	TTGGCCGGTGCTGGG
(SEQ ID NO: 81)	3'TCGGACTCACAAGGACGATTTG	AGAGTGGTCGTGAAC	CGCCACGACCC

250

HAIRPIN

FIG. 49E



L. 100. 8 -1 (SEQ ID NO: 76)	CAGAGTGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCAGCGAGGTGCGAACGAAATTTCTGGAGAAGTTATTTTCGACGC	300
L. 46.16-10 (SEQ ID NO: 77)	CAGAGTGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCAGCGAGGTGCGAACGAAATTTCTGGAGAAGTTATTTTCGACGG	
L. 46.16-12 (SEQ ID NO: 78)	CAGAGTGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCAGCGAGGTGCGAACGAAATTTCTGGAGAAGTTATTTTCGACGG	
L. 19.16-3 (SEQ ID NO: 79)	CAGAGTGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCAGCGAGGTGCGAACGAAATTTCTGGAGAAGTTATTTTCGACGG	
L. CEM/251 (SEQ ID NO: 80)	CAGAGTGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCAGCGAGGTGCGAACGAAATTTCTGGAGAAGTTATTTTCGACGG	
L. 36.8-3 (SEQ ID NO: 81)	CAGAGTGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCAGCGAGGTGCGAACGAAATTTCTGGAGAAGTTATTTTCGACGG	
HAIRPIN		

FIG. 49F

L.100.8-1	<div>350</div> <div>5'ATTTTAGAAGTAGGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG</div> <div>3'TAAATCTTCATCCGGTCACACACAAGGGTAGAGGATCGGCGCGGAC</div> <div>G 3'</div> <div>C 5'</div>
L.46.16-10	<div>5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG</div> <div>3'TAAATCTTCATTCGGTCACACACAAGGGTAGAGGATCGGCGCGGAC</div> <div>G 3'</div> <div>C 5'</div>
L.46.16-12	<div>5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG</div> <div>3'TAAATCTTCATTCGGTCACACACAAGGGTAGAGGATCGGCGCGGAC</div> <div>G 3'</div> <div>C 5'</div>
L.19.16-3	<div>5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG</div> <div>3'TAAATCTTCATCCGATCACACACAAGGGTAGAGGATCGGCGCGGAC</div> <div>G 3'</div> <div>C 5'</div>
L.CEM/251	<div>5'ATTTTAGAAGTAAGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG</div> <div>3'TAAATCTTCATTCGATCACACACAAGGGTAGAGGATCGGCGCGGAC</div> <div>G 3'</div> <div>C 5'</div>
L.36.8-3	<div>5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG</div> <div>3'TAAATCTTCATCCGATCACACACAAGGGTAGAGGATCGGCGCGGAC</div> <div>G 3'</div> <div>C 5'</div>

FIG. 49G

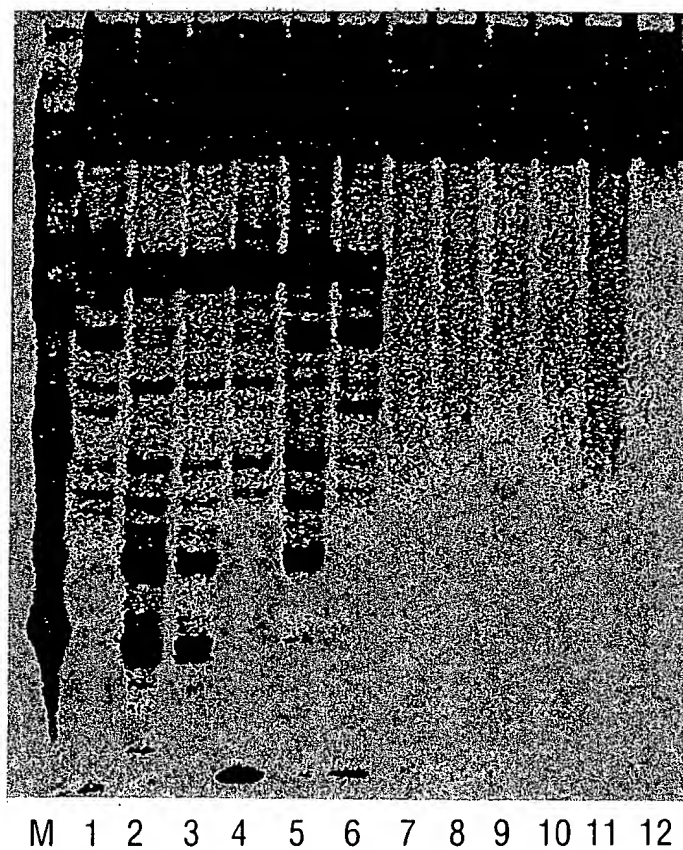
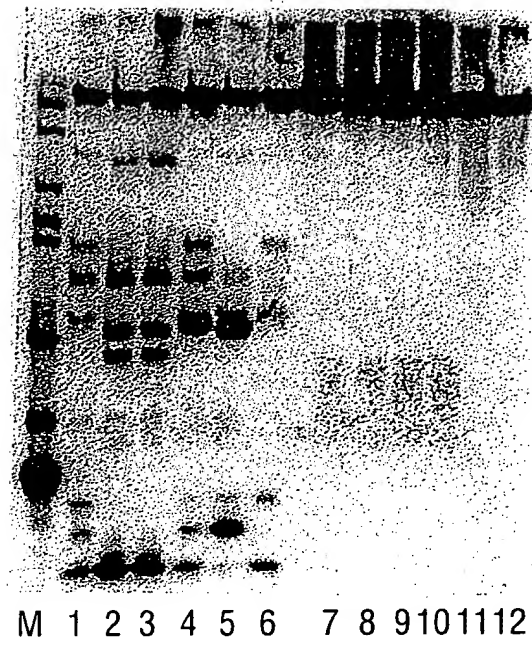


FIG. 50



**FIG. 51**

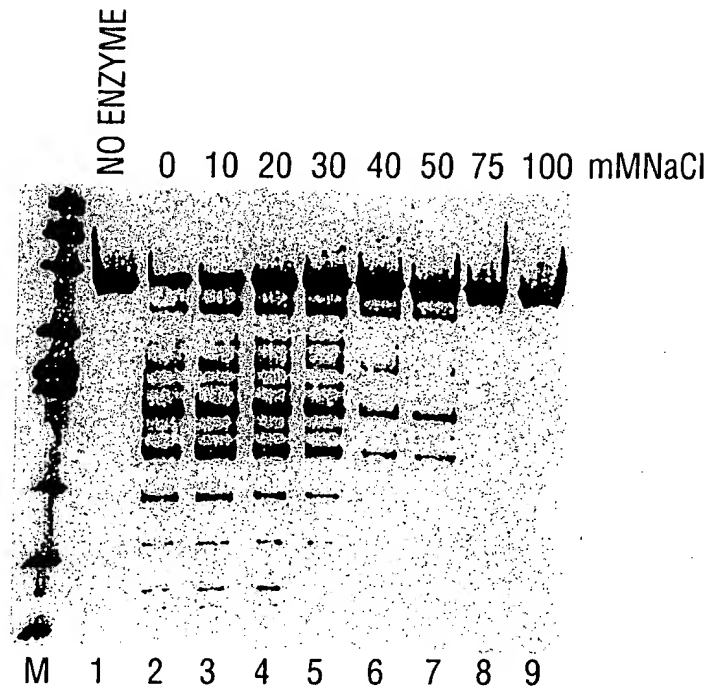
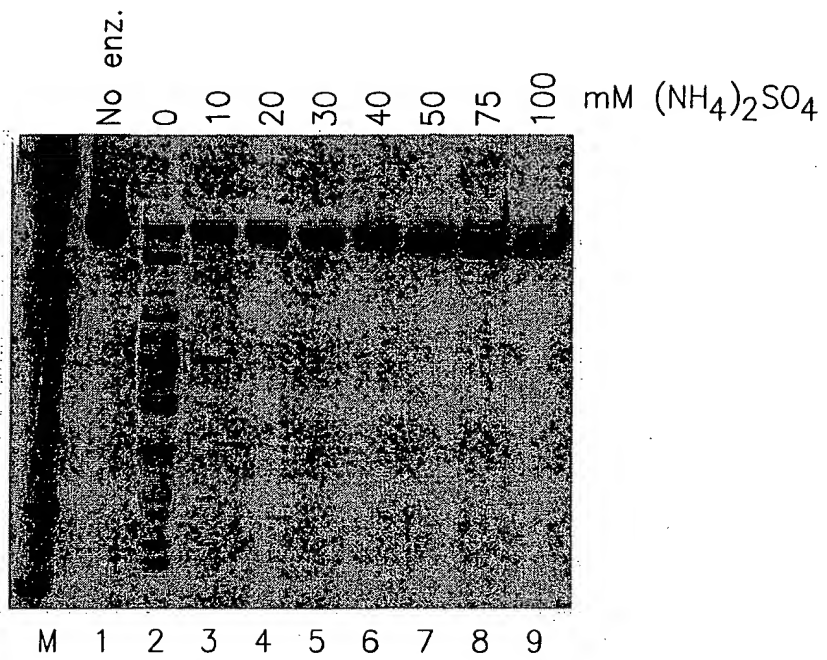
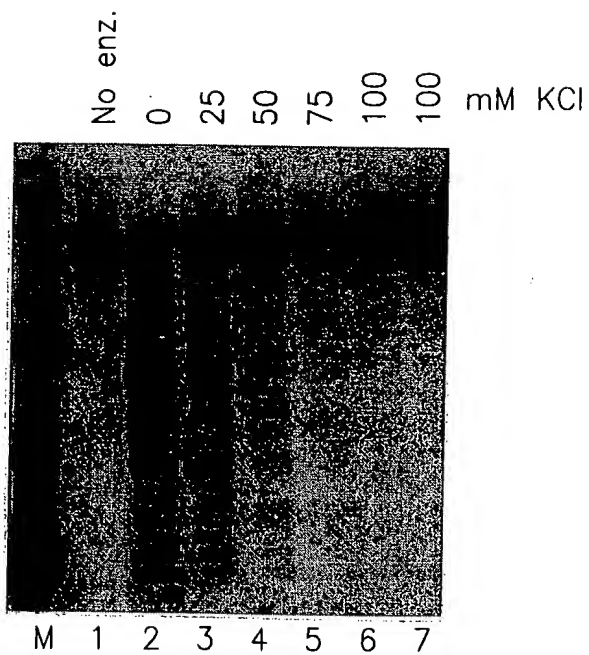


FIG. 52



**FIG. 53**



**FIG. 54**

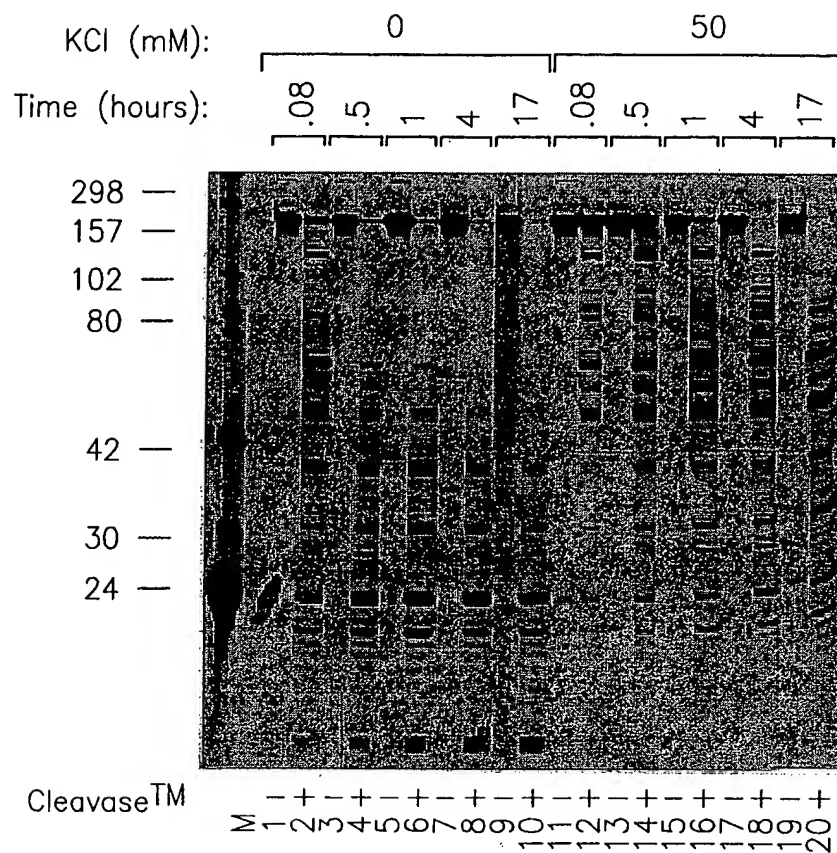


FIG. 55

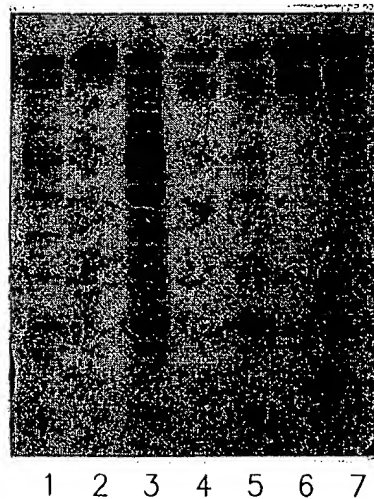


FIG. 56

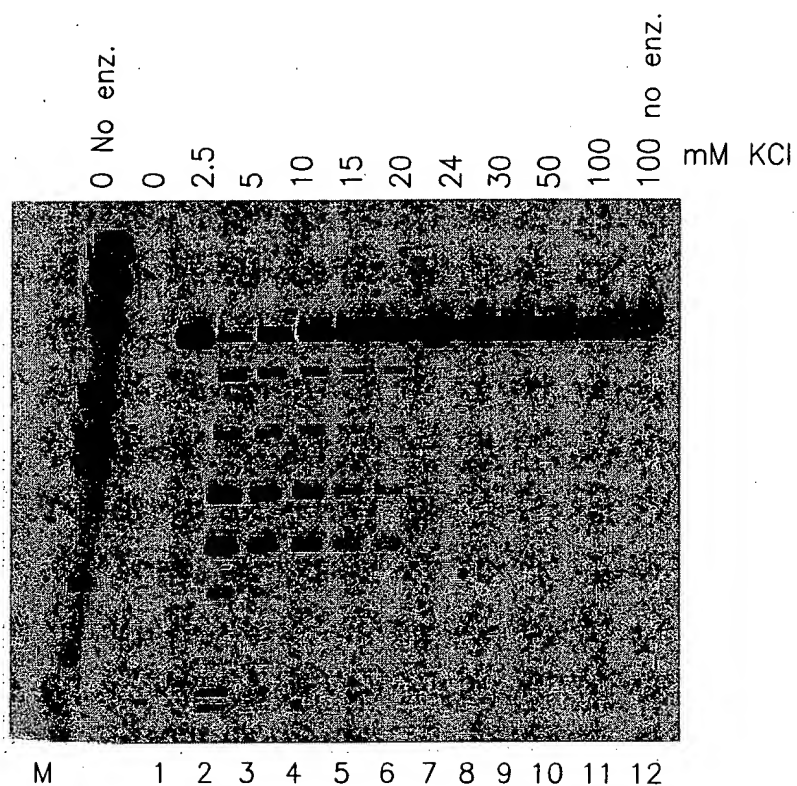


FIG. 57

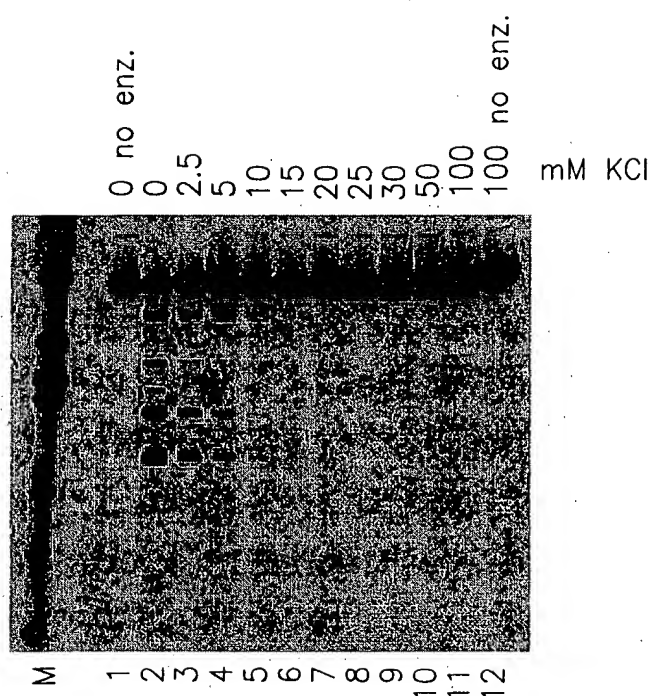


FIG. 58



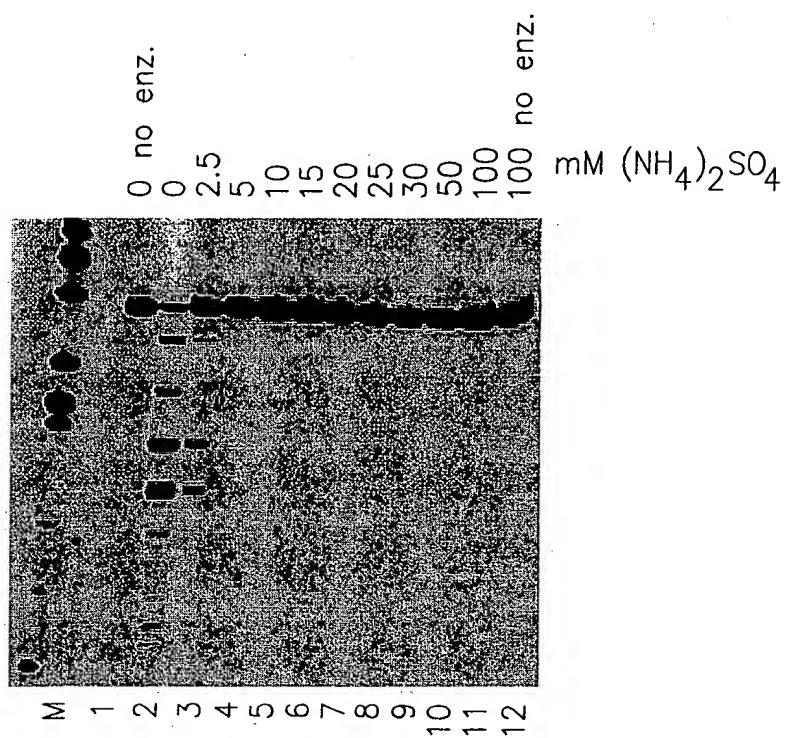


FIG. 59

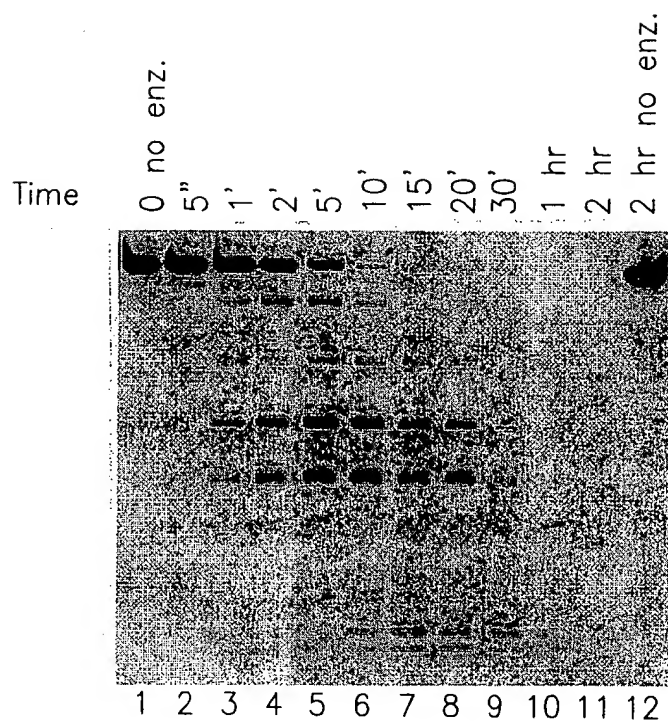


FIG. 60

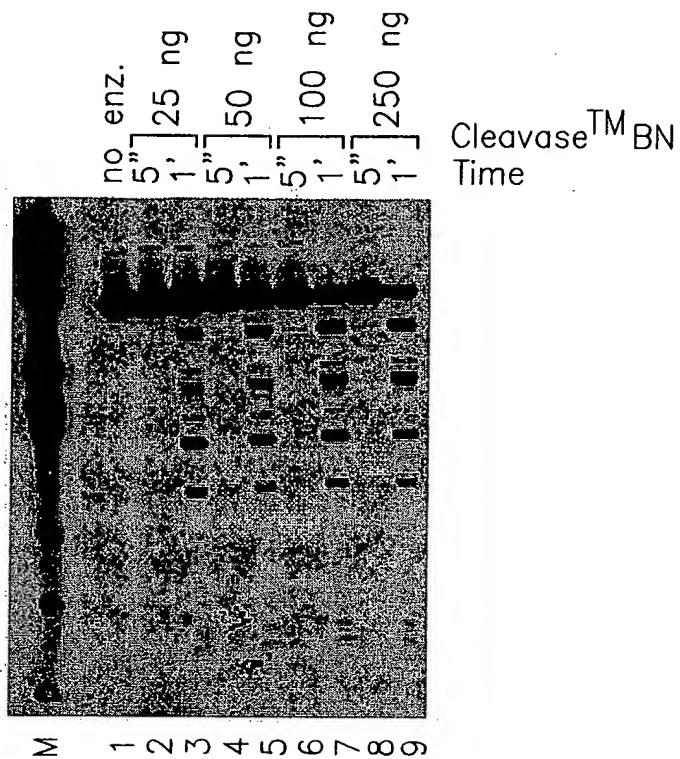


FIG. 61

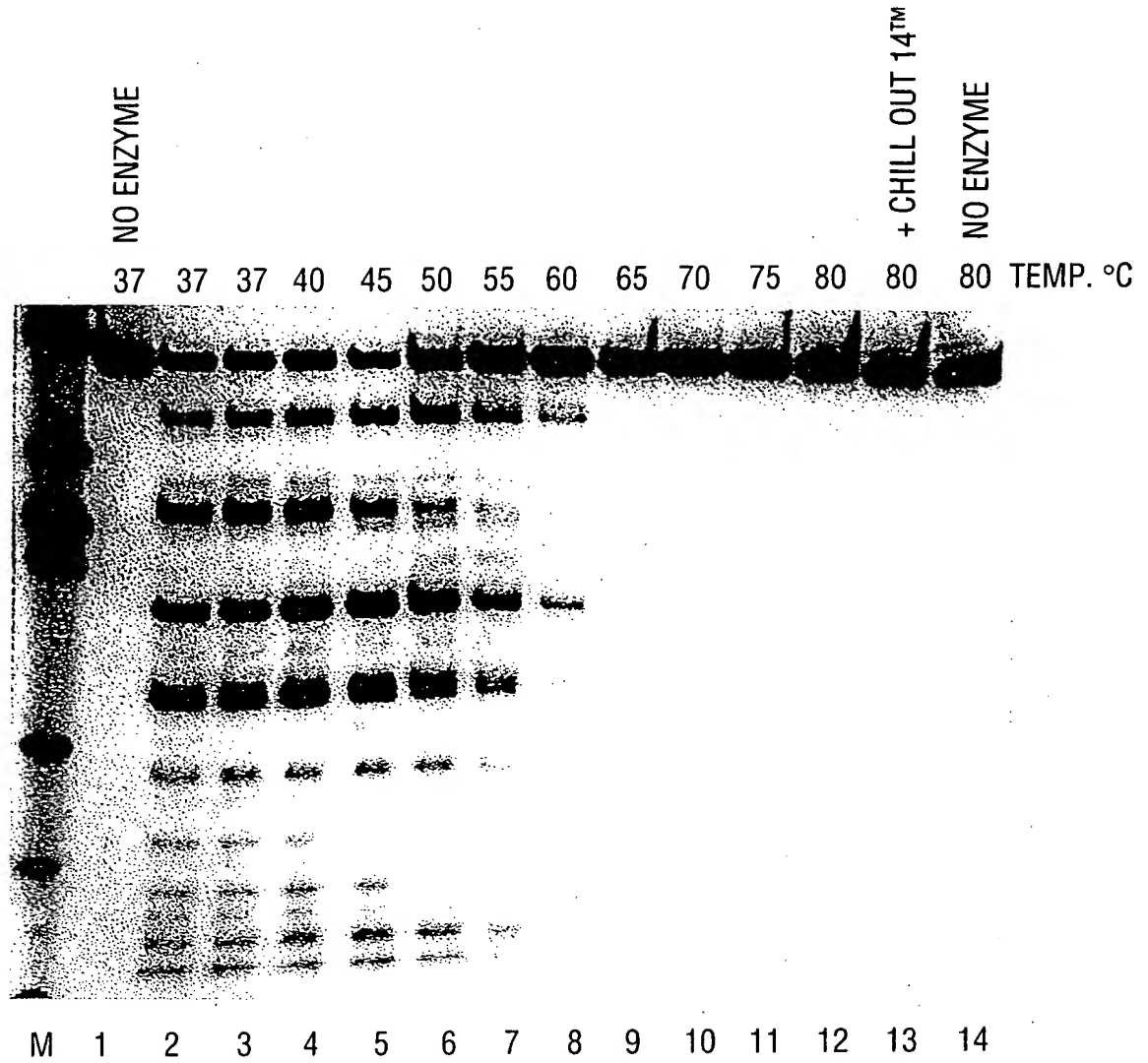


FIG. 62

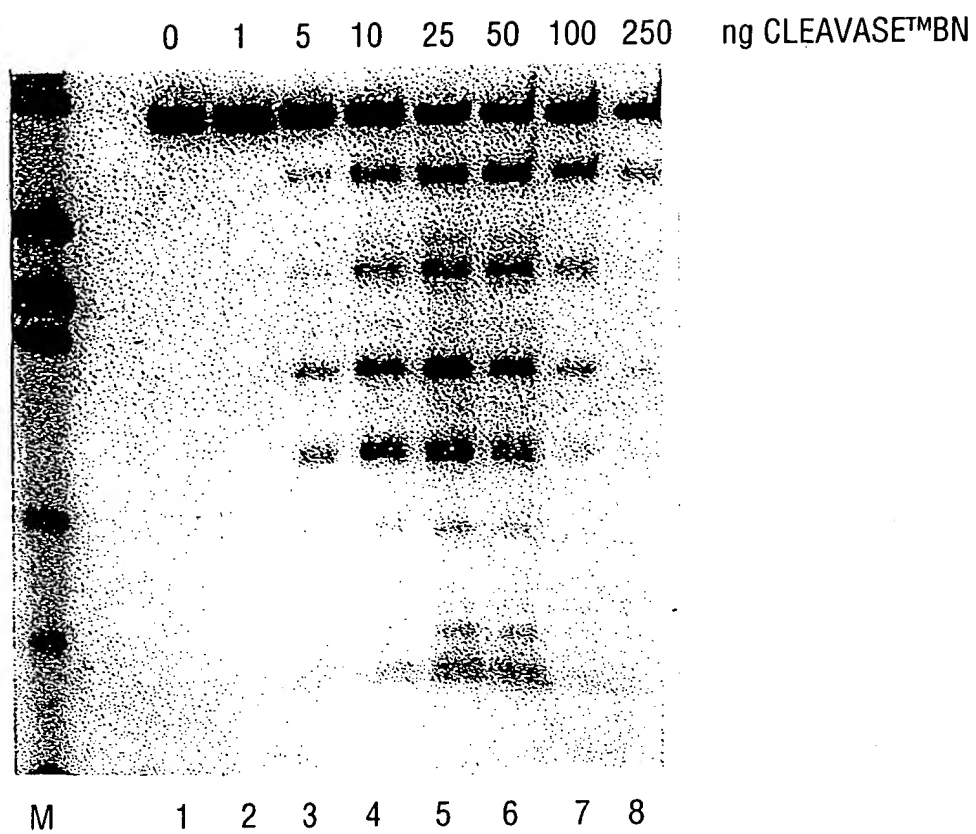
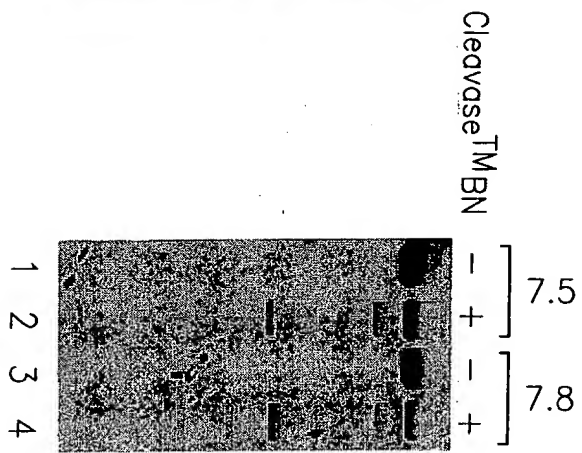
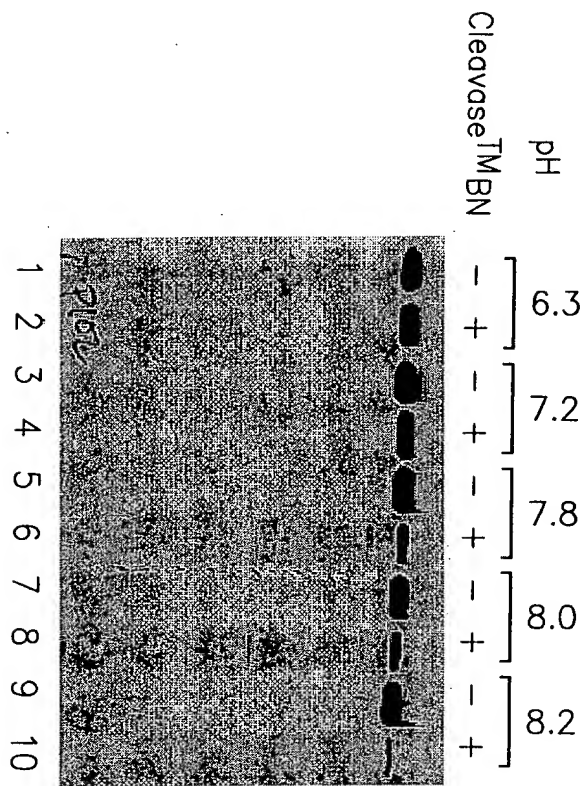


FIG. 63



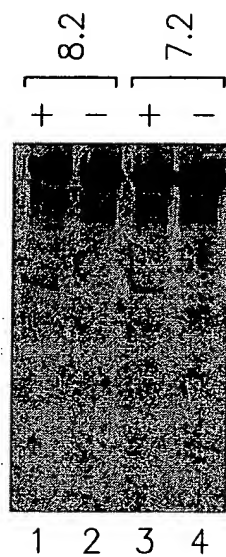


FIG. 65A

pH  
Cleavase<sup>TM</sup>BN

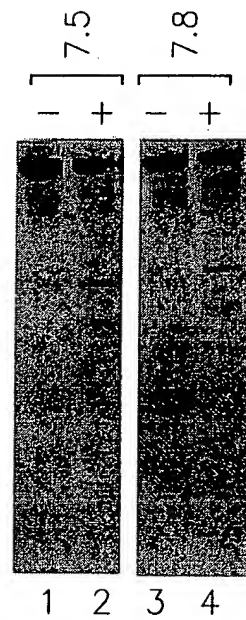


FIG. 65B

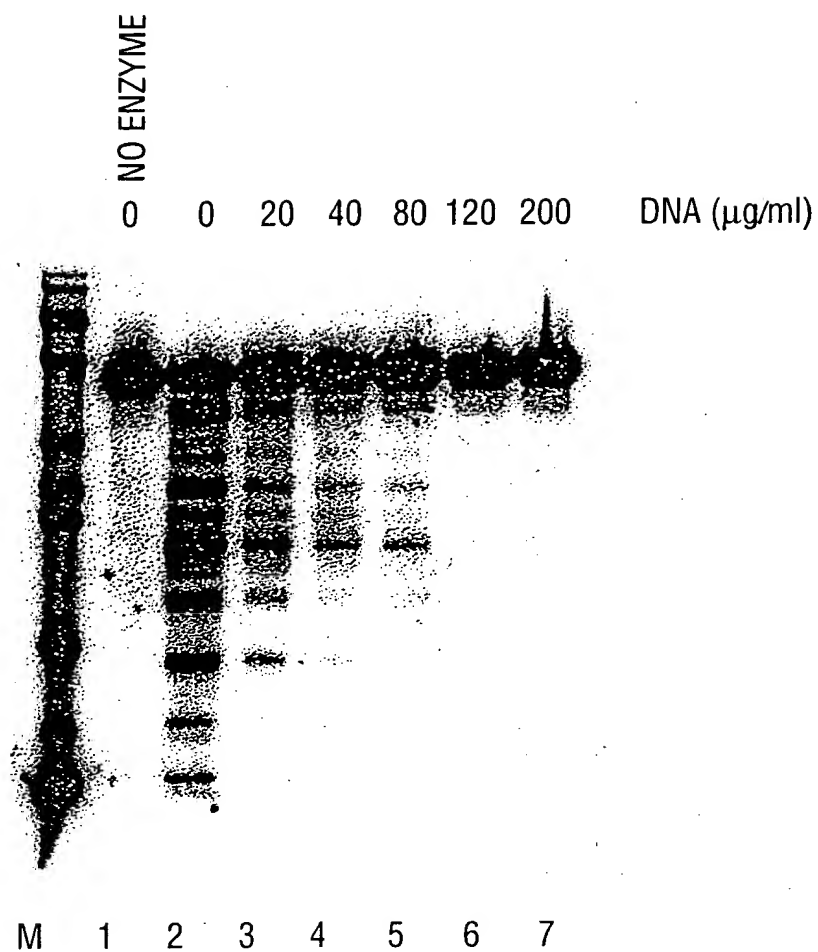
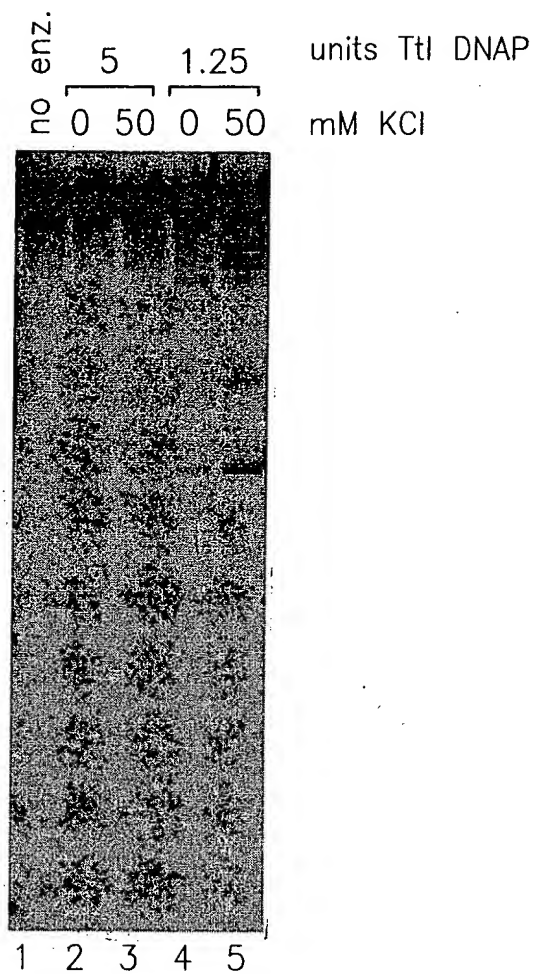
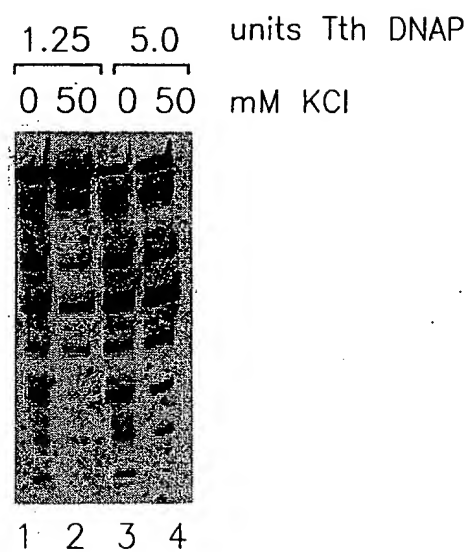


FIG. 66



**FIG. 67**



**FIG. 68**



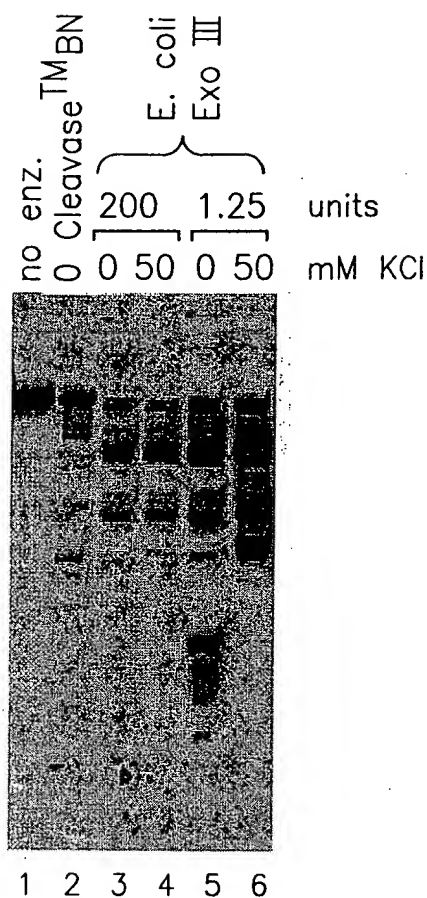


FIG. 69

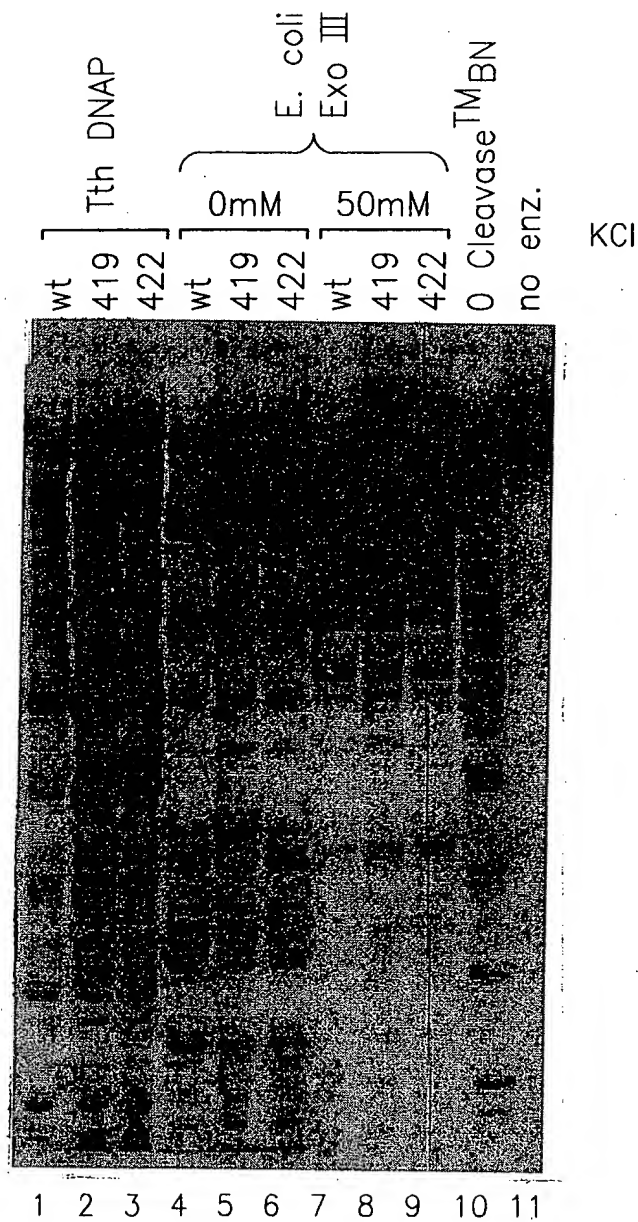
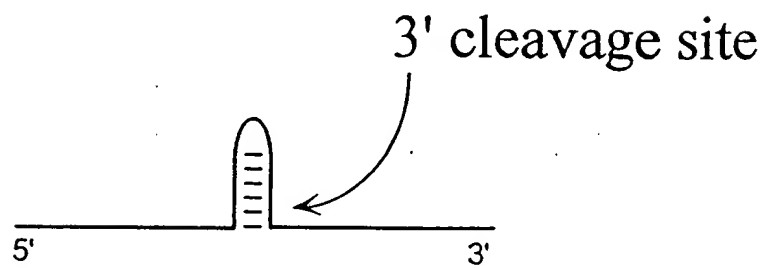
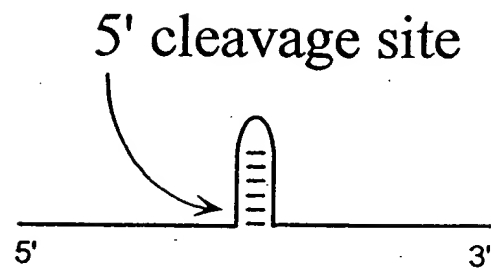
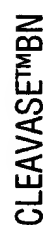


FIG. 70

**FIG. 71**

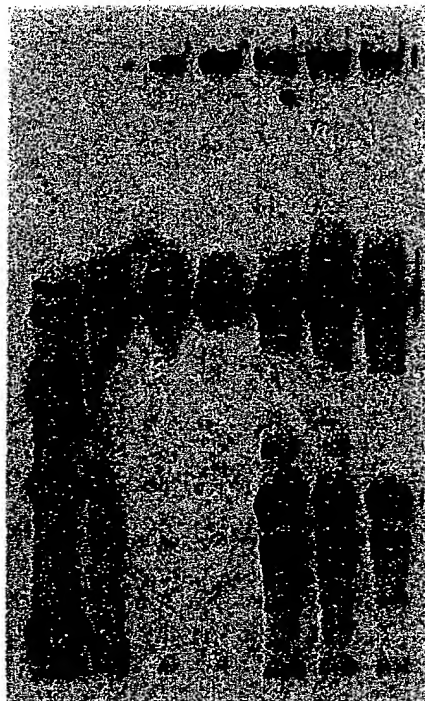




Rad 1/Rad 10

FIG. 72

174



M 1 2 3 4 5 6

**FIG. 73**

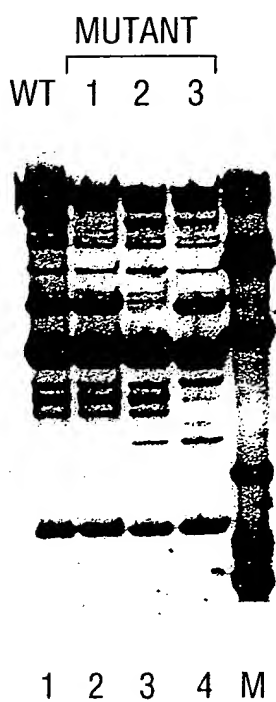


FIG. 74A

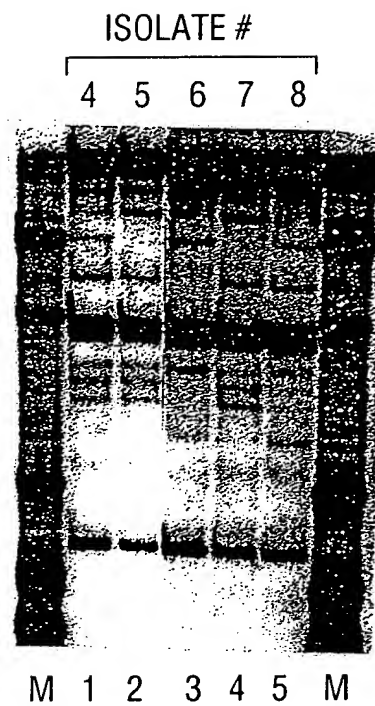
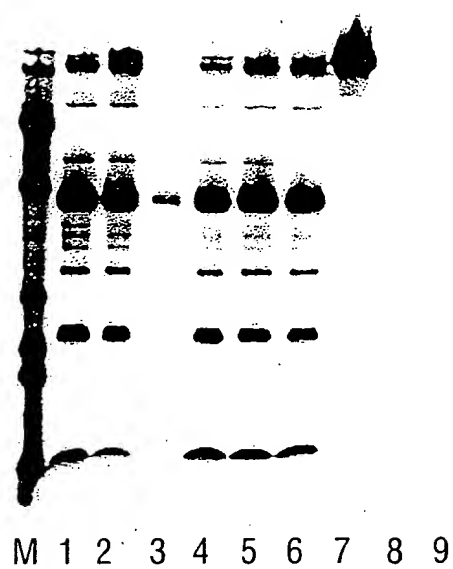


FIG. 74B



**FIG. 75**

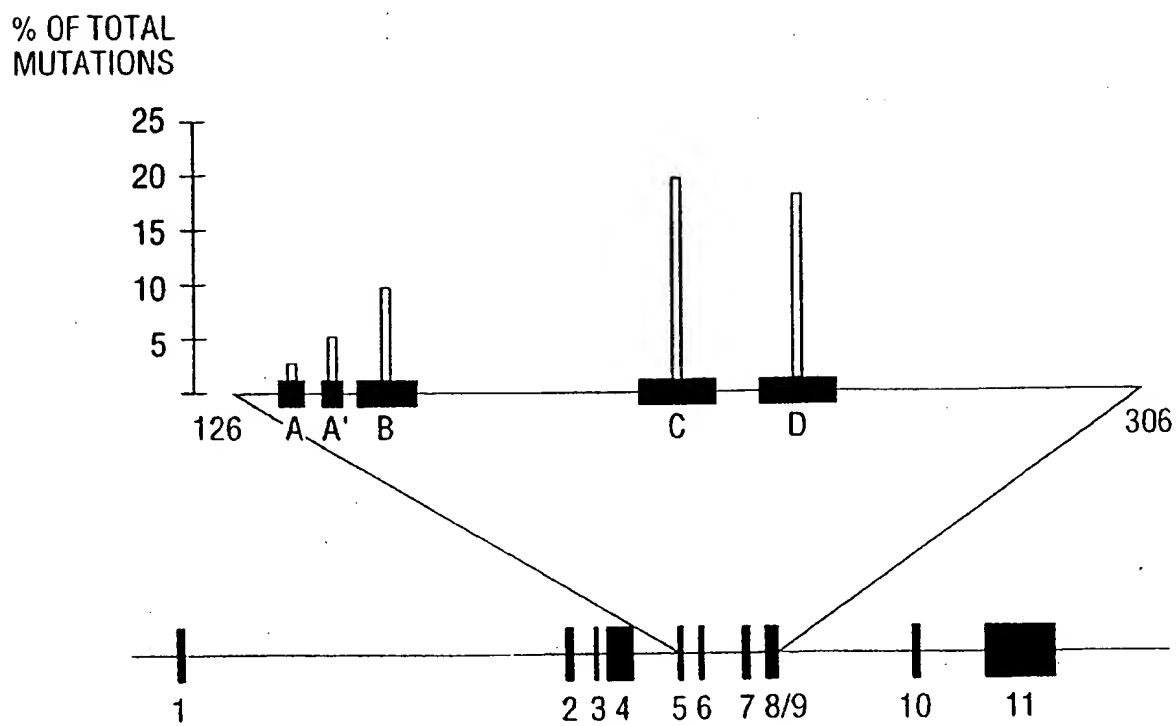


FIG. 76

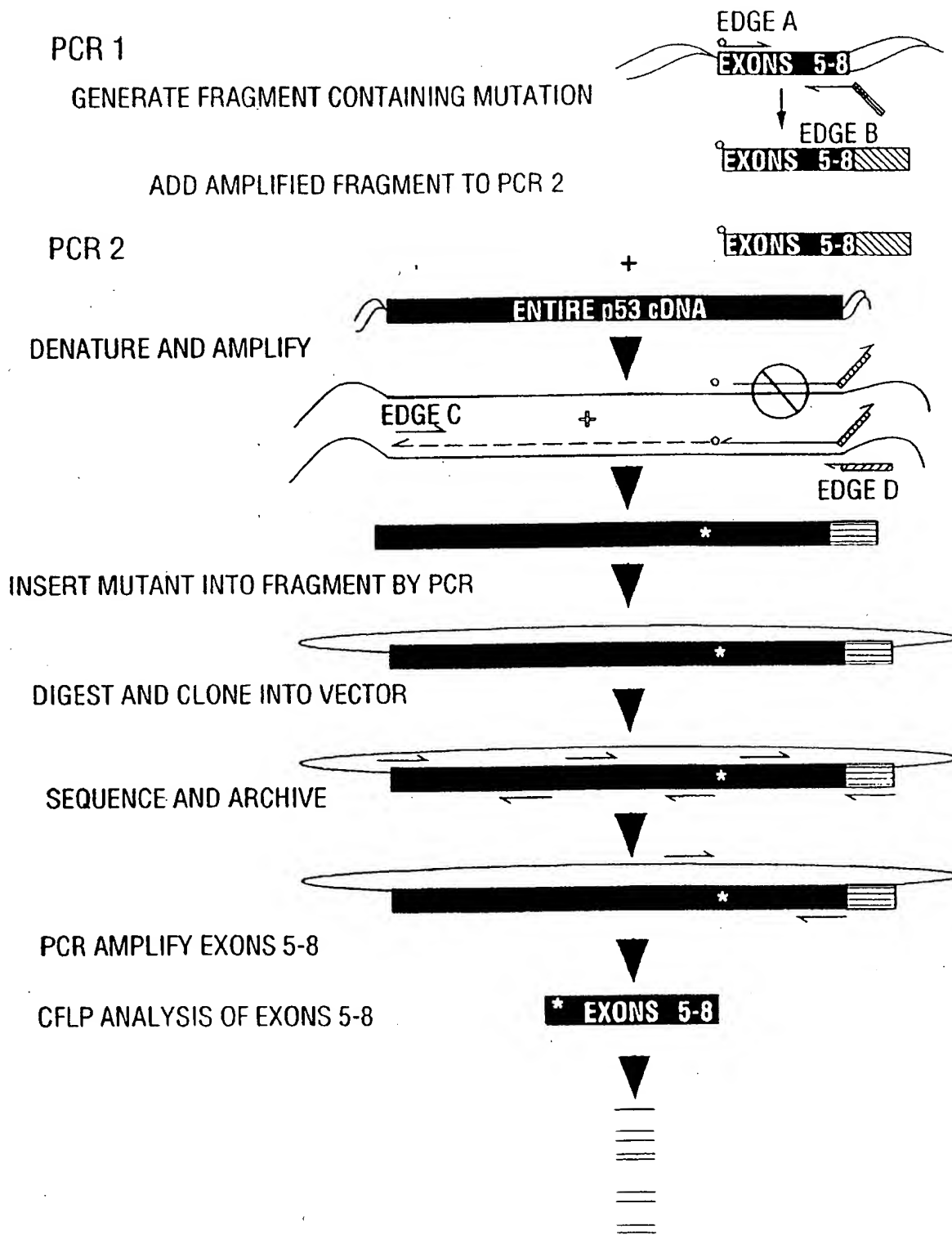


FIG. 77



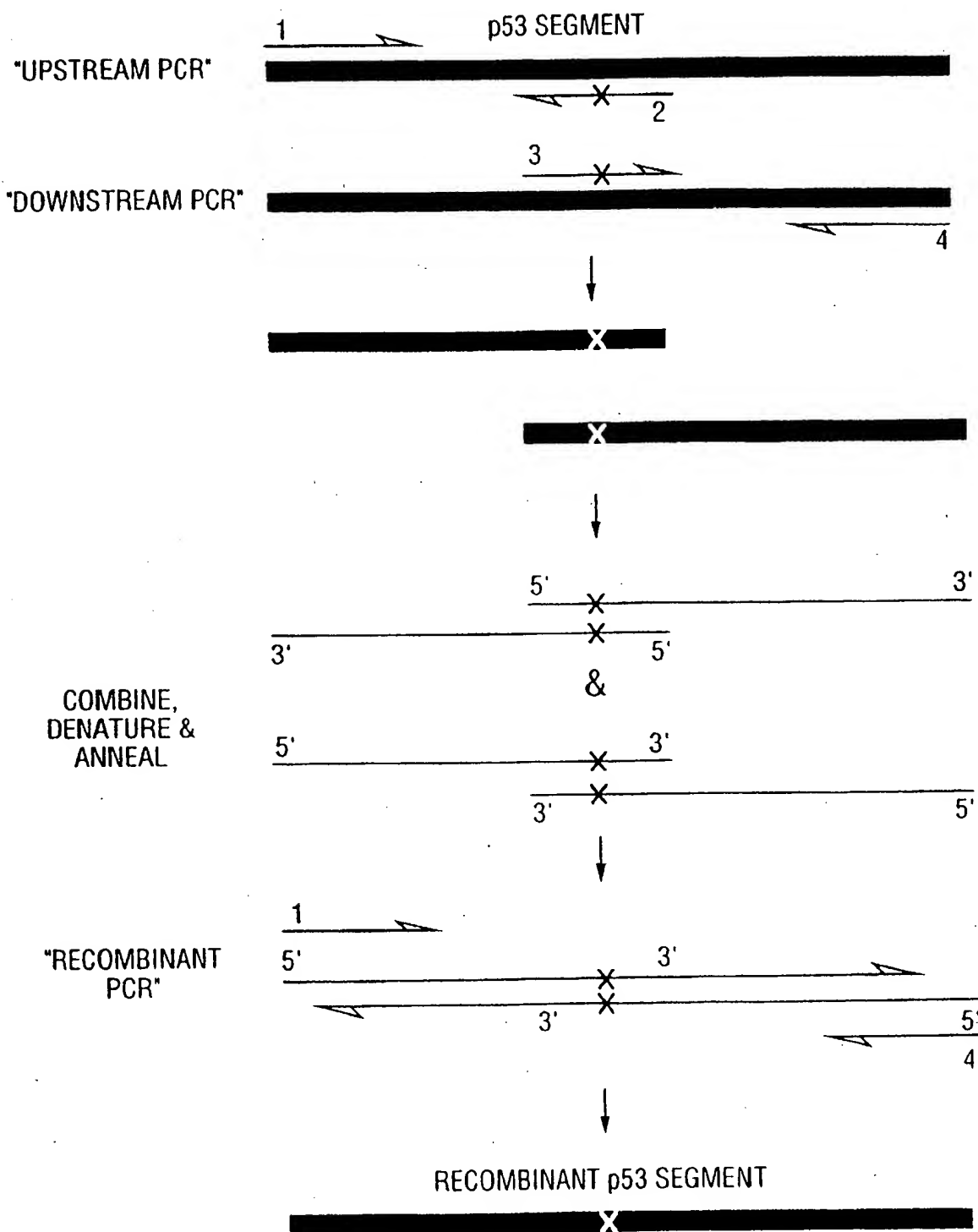


FIG. 78

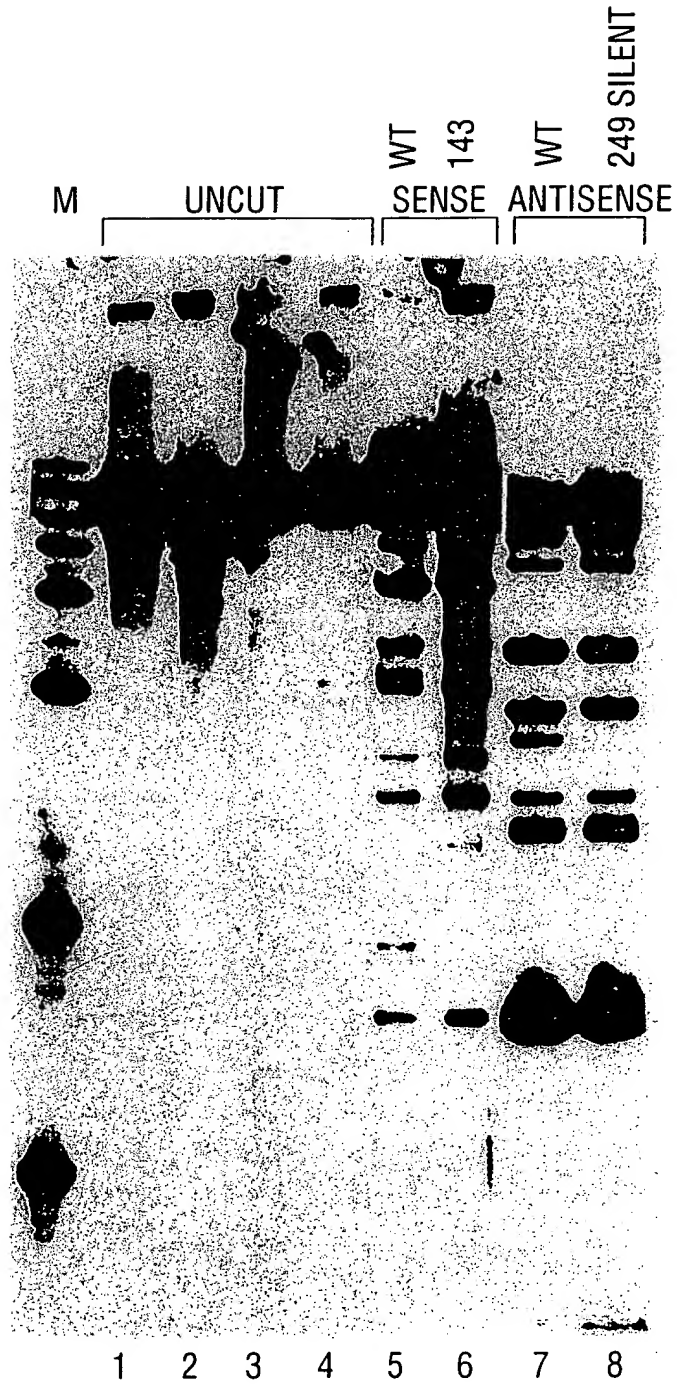


FIG. 79

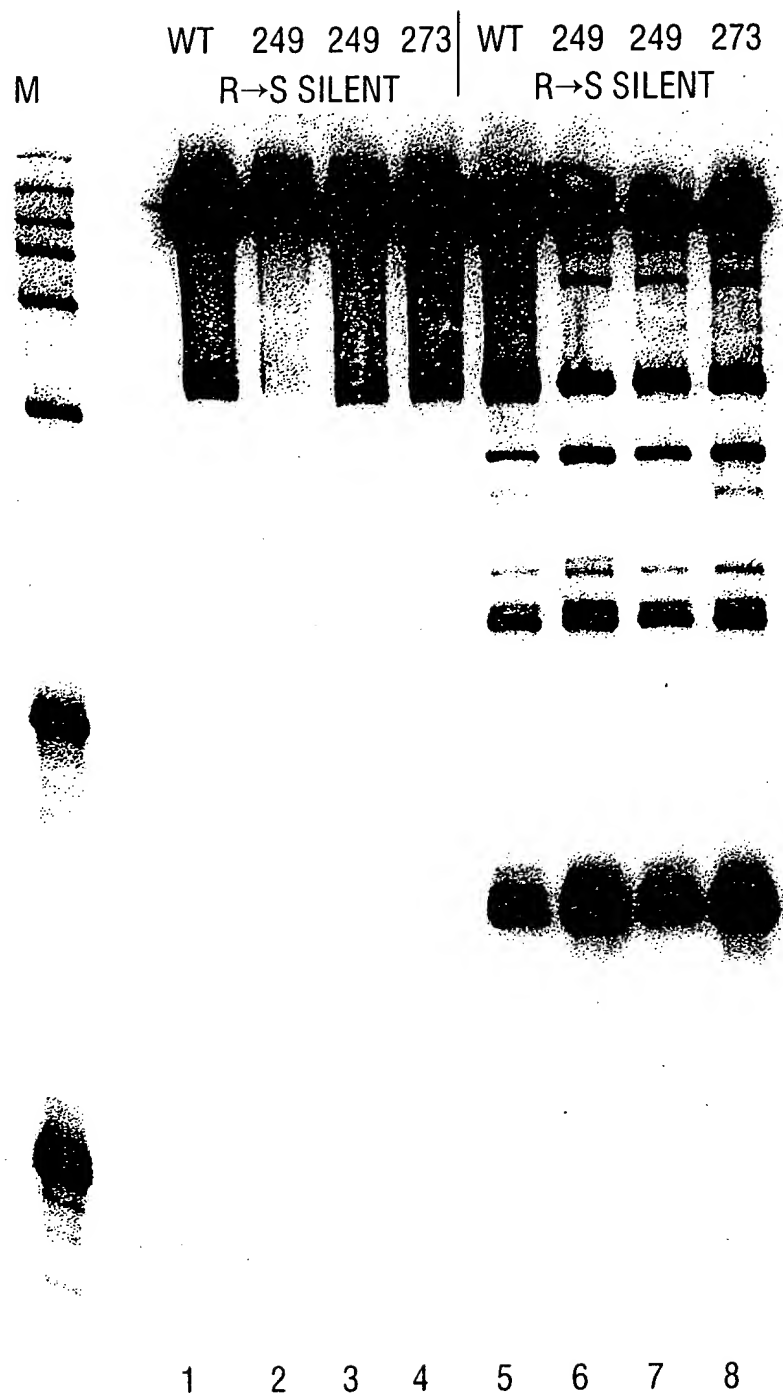


FIG. 80

MIXING PROPORTIONS

M	UNCUT	1	1	1	1	0	2	4	9	WILD TYPE
	WT MUT	0	1	2	9	1	1	1	1	MUTANT

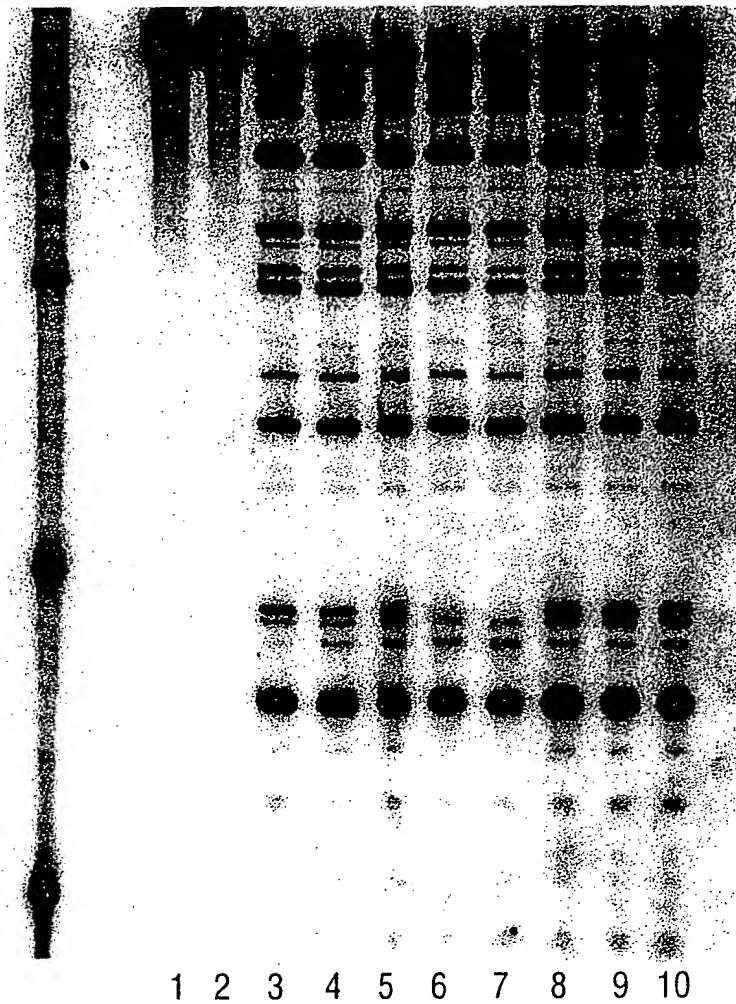


FIG. 81

FIG. 82

HCV1.1	(SEQ ID NO:121)	1	CTGTCTTCAC	GCAGAAAGCG	TCTGGCCATG	GCGTTAGTAT	GAGTGTGCTG	50
HCV2.1	(SEQ ID NO:122)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTGCTG	
HCV3.1	(SEQ ID NO:123)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTGCTG	
HCV4.2	(SEQ ID NO:124)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTGCTG	
HCV6.1	(SEQ ID NO:125)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTGCTG	
HCV7.1	(SEQ ID NO:126)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTGCTG	
HCV1.1		51	CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGT	CTGCCGAACC	100
HCV2.1			CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGT	CTGCCGAACC	
HCV3.1			CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGT	CTGCCGAACC	
HCV4.2			CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGT	CTGCCGAACC	
HCV6.1			CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGT	CTGCCGAACC	
HCV7.1			CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGT	CTGCCGAACC	
HCV1.1		101	GGTAGTACA	CCGGAATTGC	CAGGACGACC	GCGTCCTTC	TTGGAT-AAA	150
HCV2.1			GGTAGTACA	CCGGAATTGC	CAGGACGACC	GCGTCCTTC	TTGGAT-CAA	
HCV3.1			GGTAGTACA	CCGGAATTGC	CAGGACGACC	GCGTCCTTC	TTGGAT-CAA	
HCV4.2			GGTAGTACA	CCGGAATTGC	CAGGACGACC	GCGTCCTTC	TTGGAT-CAA	
HCV6.1			GGTAGTACA	CCGGAATTGC	CAGGACGACC	GCGTCCTTC	TTGGAT-CAA	
HCV7.1			GGTAGTACA	CCGGAATTGC	CAGGACGACC	GCGTCCTTC	TTGGAT-CAA	
HCV1.1		151	CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	200
HCV2.1			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV3.1			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV4.2			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV6.1			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV7.1			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV1.1		201	AGTAGTGTG	GGTCGCGAAA	GCGCTTGTG	TACTGCTGA	TAGGCTGCTT	250
HCV2.1			AGTAGTGTG	GGTCGCGAAA	GCGCTTGTG	TACTGCTGA	TAGGCTGCTT	
HCV3.1			AGTAGTGTG	GGTCGCGAAA	GCGCTTGTG	TACTGCTGA	TAGGCTGCTT	
HCV4.2			AGTAGTGTG	GGTCGCGAAA	GCGCTTGTG	TACTGCTGA	TAGGCTGCTT	
HCV6.1			AGTAGTGTG	GGTCGCGAAA	GCGCTTGTG	TACTGCTGA	TAGGCTGCTT	
HCV7.1			AGTAGTGTG	GGTCGCGAAA	GCGCTTGTG	TACTGCTGA	TAGGCTGCTT	
HCV1.1		251	GCGAGTGCC	CGGAGGTCT	CGTAGACCGT	GC	282	
HCV2.1			GCGAGTGCC	CGGAGGTCT	CGTAGACCGT	GC		
HCV3.1			GCGAGTGCC	CGGAGGTCT	CGTAGACCGT	GC		
HCV4.2			GCGAGTGCC	CGGAGGTCT	CGTAGACCGT	GC		
HCV6.1			GCGAGTGCC	CGGAGGTCT	CGTAGACCGT	GC		
HCV7.1			GCGAGTGCC	CGGAGGTCT	CGTAGACCGT	GC		

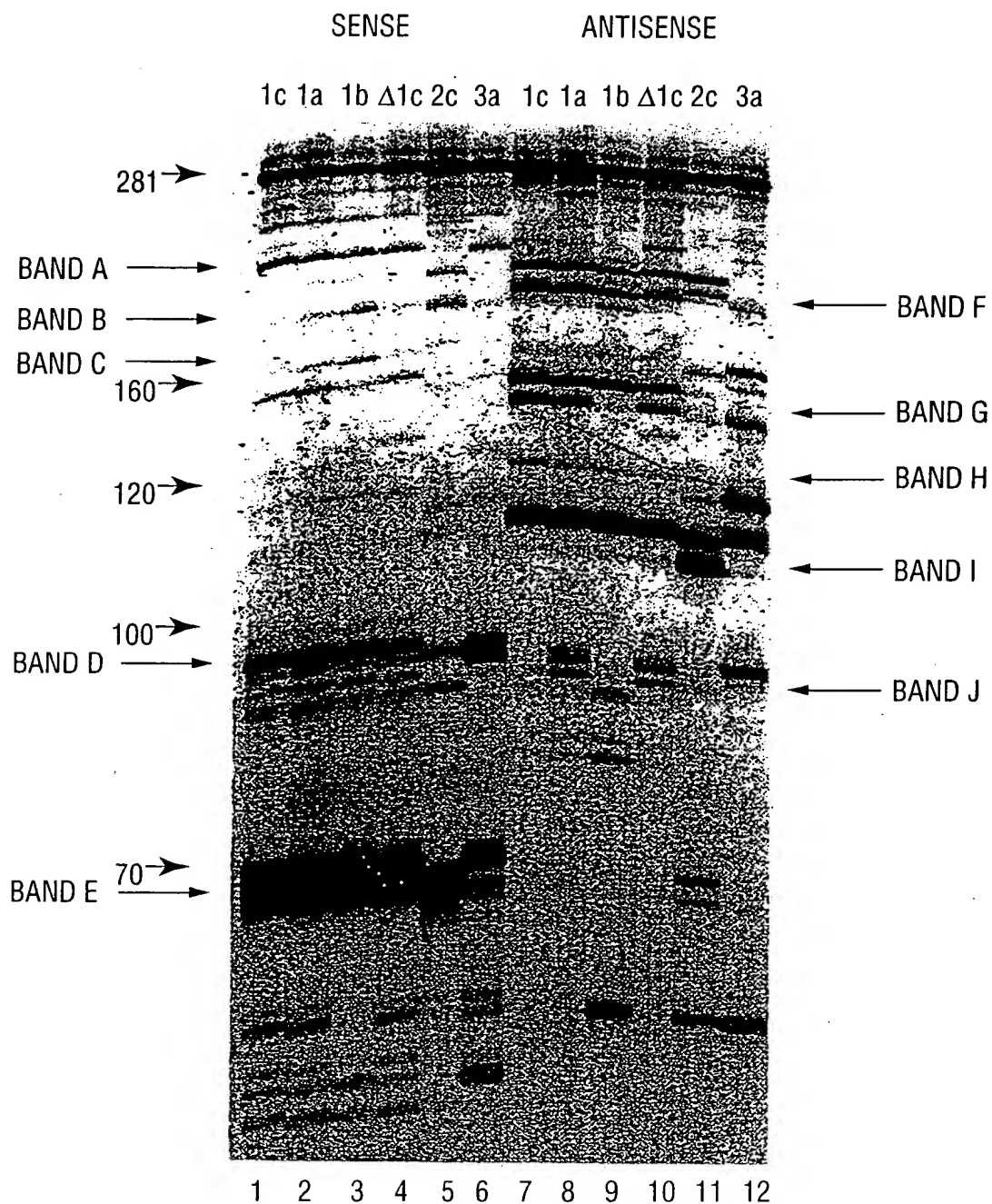


FIG. 83

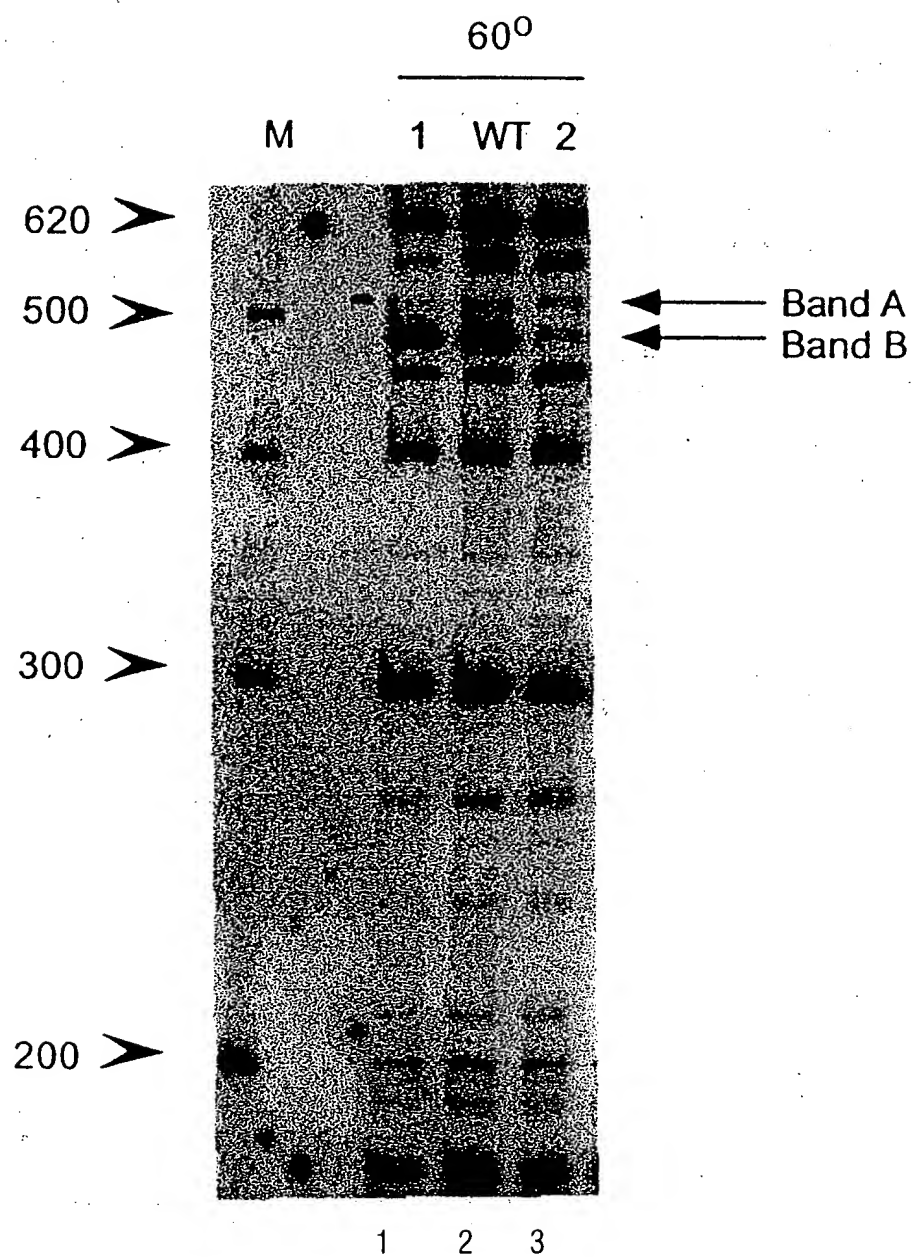


FIG. 84

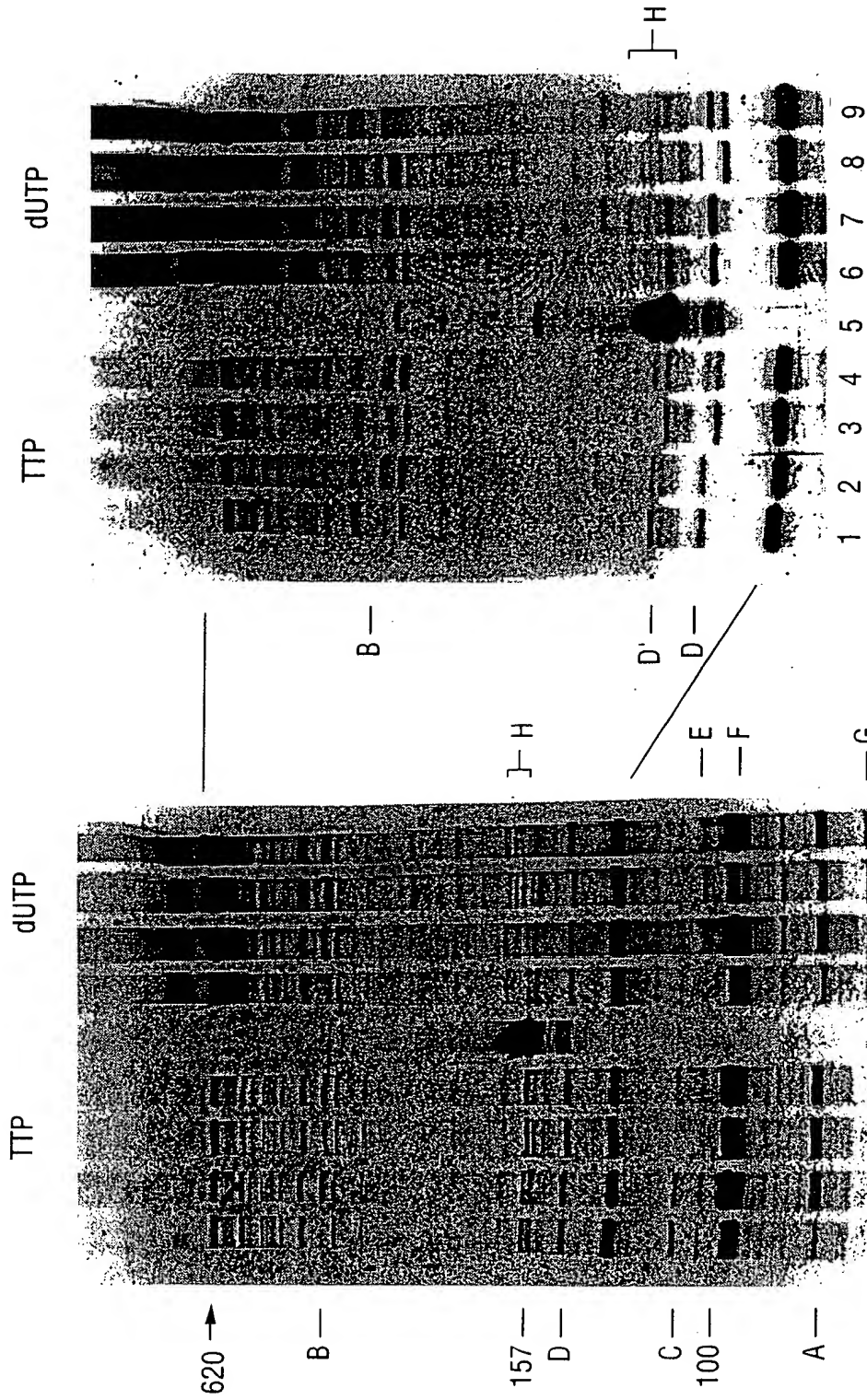


FIG. 85B

FIG. 85A



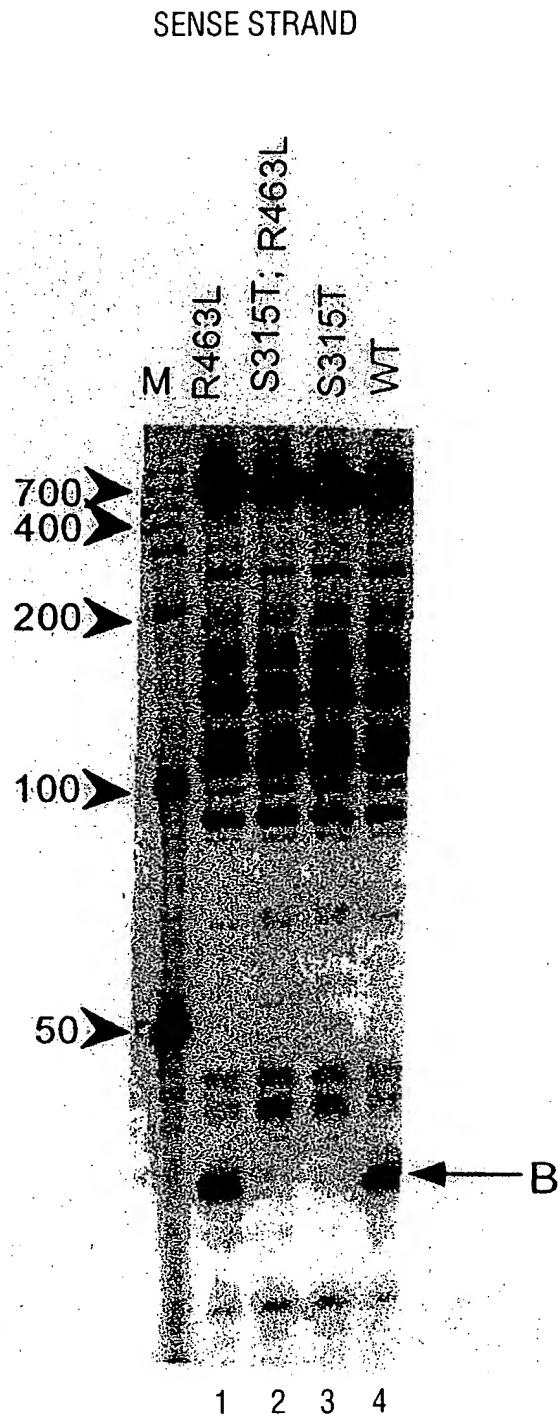
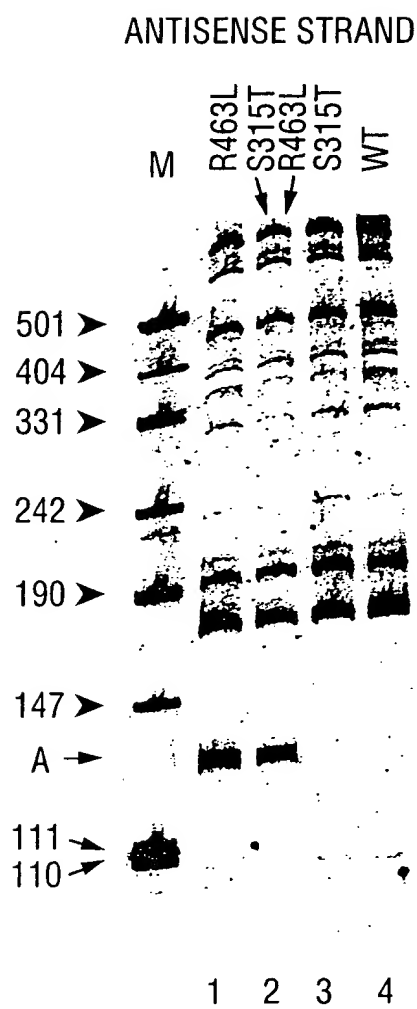


FIG. 86



**FIG. 87**

10	20	30	40	50	60	
AGA GTT	GATCCT	GGCTCAG				
AAATTGA	<u>AGAG</u>	GTTGATCAI	GGCTCAGATT	GAACGCTGGC	GGCAGGCCCTA	ACACATGCAA
TTTA	ACTTCT	CAA	ACTAGTA	CCGAGTCTAA	CTTGCGACCG	CCGTCCGGAT
						TGTGTACGTT
70	80	90	100	110	120	
GTCGAACGGT	AACAGGAAGA	AGCTTGCTTC	TTTGCTGACG	AGTGGCGGAC	GGGTGAGTAA	
CAGCTTGECA	TTGTCCTTCT	TCGAACGAAG	AAACGACTGC	TCACCGCCTG	CCCACCTCAT	
						ER10
130	140	150	160	170	180	
TGCTCTGGGAA	ACTGCCTGAT	GGAGGGGGAT	AACTACTGGA	AACGGTAGCT	AATACCGCAT	
ACAGACCCCTT	TGACGGACTA	CCTCCCCCTA	TTGATGACCT	TTGCCATCGA	TTATGGCGTA	
190	200	210	220	230	240	
AACGTCGCAA	GACCAAGAGAG	GGGACCTTTC	GGGCTCTTTG	CCATCGGATG	TGCCCAGATG	
TTGCAGCGTT	CTGGTTTCTC	CCCCTGGAAG	CCCGGAGAAC	GGTAGCCTAC	ACGGGTCTAC	
250	260	270	280	290	300	
GGATTAGCTA	GTAGGTGGGG	TAACGGCTCA	CCTAGGCGAC	GATCCCTAGC	TGGTCTGAGA	
CCTAATCGAT	CATCCACCCC	ATTGCCGAGT	GGATCCGCTG	CTAGGGATCG	ACCAGACTCT	
310	320	330	340	350	360	
GGATGACCCAG	CCACACTGGA	ACTGAGACAC	GGTCCAGACT	CCTACGGGGAG	GCAGCAGTGG	
CCTACTGGTC	GGGTGACCT	TGACTCTGTG	CCAGGTCTGA	GGATGCCCTTC	CGTGGTACCC	
						1659
						TGA GGATGCCCTTC CGTCGTC

FIG. 88A

370	380	390	400	410	420
GGAATATTGC	ACCAATGGCG	CAAGCCTGAT	GCAGCCATGC	CGCGTGTATG	AAGAAGGCCCT
CCTTATAACG	TGTTACCCCG	GTTCCGACTA	CGTCGGTACG	GGCACAATAC	TTCCTCCGGA
430	440	450	460	470	480
TCGGGTTGTA	AAGTACTTTC	AGCGGGGAGG	AAGGAGTAA	AGTTAATACC	TTTGCTCATT
AGCCCAACAT	TTCAATGAAG	TCGCCCCCTC	TTCCCTCATT	TCAATTATGG	AAACGAGTAA
490	500	510	520	530	540
GACGTTACCC	GCAGAAGAAG	CACCGGCTAA	CTCCGTGCCA	GCAGCCGCGG	TAATACGGAG
CTGCAATGGG	CGTCTTCTTC	GTGGCCGATT	GAGGCACGGT	CGTCGGCGCC	ATTATGCCCTC
550	560	570	580	590	600
GGTGCAAGCG	TTAATCGGAA	TTACTGGGCG	TAAAGCGCAC	GCAGCGGTTT	TGTTAAGTCA
CCACGTTCCG	AATTAGCCTT	AATGACCCGC	ATTTCGGGTG	CGTCCGCCAA	ACAATTTCAGT
610	620	630	640	650	660
GATGTGAAAT	CCCCGGGCTC	AACCTGGGAA	CTGCATCTGA	TACTGGCAAG	CTTGAGTCTC
CTACACTTTA	GGGGCCCCGAG	TTGGACCCCT	GACGTAGACT	ATGACCGTTC	GAACTCAGAG
670	680	690	700	710	720
GTAGAGGGGG	GTAGAATTCC	AGGTGTAGCG	GTGAAATGCC	TAGAGATCTC	GAGGAATACC
CATCTCCCCC	CATCTTAAGG	TCCACATCGC	CACCTTACGC	ATCTCTAGAC	CTCCTTATGG
730	740	750	760	770	780
GGTGGCGAAG	GGGGCCCCCT	GGACGAAGAC	TGACGCTCAG	GTGCGAAAGC	GTGGGGAGCA
CCACCGCTTC	CGCCGGGGGA	CCTGCTTCTG	ACTGCGAGTC	CACGCTTTCC	CACCCCTCGT

**FIG. 88B**

790	800	810	820	830	840
AACAGGATTA	GATACCCCTGG	TAGTCCACGC	CGTAACCGAT	GTGACCTGG	AGGTTGTGCC
TTGTCCTAAT	CTATGGGACC	ATCAGGTGCG	GCAATTGGCTA	CAGCTGAACC	TCCACACACGG
850	860	870	880	890	900
CTTGAGGCGT	GGCTTCCGGA	GCTAACGCGT	TAAGTCGACC	GCCTGGGGAG	TACGGCCGCA
GAACTCCGCA	CCGAAGGCTT	CGATTGCGCA	ATTCAGCTGG	CGGACCCCTC	ATGCCGGCGT
910	920	930	940	950	960
AGGTTAAAC	TCAAATGAAT	TGAGGGGGGC	CCGCACCAAGC	GGTGAGCAT	GTGGTTAAT
TCCAATTTTG	AGTTACTTA	ACTGCCCCCG	GGCGTGTTCG	CCACCTCGTA	CACCAAAATTA
970	980	990	1000	1010	1020
TCGATGCAAC	GGGAAGAACC	TTACCTGGTC	TTGACATCCA	CGGAAGTTT	CAGAGATGAG
AGCTACGTTG	CGCTTCTTGG	AATGGACCAG	AACTGTAGGT	GCCTTCAAAA	GTCTCTACTC
1030	1040	1050	1060	1070	1080
AATGTGCCTT	CGGGAACCGT	GAGACAGGTG	CTGCATGGCT	GTGTCAGCT	CGTGTGTGA
TTACACGGAA	GCCCCTTGGCA	CTCTGTCCAC	GACGTACCGA	CAGCAGTCGA	GCACACACACT
1090	1100	1110	1120	1130	1140
	GC	AACGAGCGCA	ACCC		
AATGTTGGGT	TAAGTCCCGC	AACGAGCGCA	ACCCCTTATCC	TTGTGCGCA	GGGTCGGGC
TTACAACCCA	ATTCAGGGCG	TTGCTCGCGT	TGGGAATAGG	AAACAACGGT	CGCCAGGCGC
1150	1160	1170	1180	1190	1200
				ATG	ACGTCAAGTC
				ATG	ACGTCAAGTC
CGGGAACCTCA	AAGGAGACTG	CCAGTGATAA	ACTGGAGGAA	GGTGGGATG	ACGTCAGTTC
GCCCTTGAGT	TTCCTCTGAC	GGTCACTAAT	TGACCTCCTT	CCACCCCTAC	TGCAGTTTCA

FIG. 88C

SB-1

SB-3  
SB-4

SB-3  
SB-4

1210	1220	1230	1240	1250	1260
ATCATGGCCC TTA					
ATCATGGCCC TTACGA					
<u>ATCATGGCCC</u> <u>TTACGACCAG</u>					
TAGTACC6GGG AATGCTGGTC	GGCTACACAC	GTGCTACAAT	GGCGCATACA	AAGAGAAGCG	
	CCGATGTGTG	CACGATGTTA	CCGCGTATGT	TTCTCTTCGC	
1270	1280	1290	1300	1310	1320
ACCTCGCGAG AGCAAGCGGA	CCTCATAAAG	TGCGTCGTAG	TCCGGATTGG	AGTCTGCAAC	
TGGAGCGCTC TCGTTCGCCT	GGAGTATTTC	ACGCAGCATC	AGGCCTAACC	TCAGACGTTG	
1330	1340	1350	1360	1370	1380
TCGACTCCAT GAAGTCGGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATACGT	
AGCTGAGGTA CTTCAGCCTT	AGCGATCATT	AGCACCTAGT	CTTACGGTGC	<u>CACCTATGCA</u>	
			GC	CACCTATGCA	

1743

1390	1400	1410	1420	1430	1440
TCCCCGGCCT TGTACACACC	GCCCCGTCACA	CCATGGGAGT	GGGTGCAAA	AGAAAGTAGT	
<u>AGGGCCCGGA</u> <u>ACATGTGTGG</u>	CGGGCAGTGT	GGTACCCCTCA	CCCAACGTTT	TCTTCATCCA	
AGGGCCCGGA ACATG					

1743

1450	1460	1470	1480	1490	1500
AGCTTAACCT TCGGGAAGGC	GCTTACCACCT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA	
TCGAATTGGA AGCCCTCCCG	CGAATGGTGA	AACACTAAGT	ACTGACCCCA	CTTCAGCATT	
1510	1520	1530	1540	1550	
CAAGGTAACC GTAGGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA.....		
GTTCCATTGG CATCCCCCTTG	GACGCCCAAC	TAGTGAGGGA	AT.....		

FIG. 88D

```

1638 (SEQ ID NO:151)
E.colirre(SEQ ID NO:158) 0 ..AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCCTAACACATGCA
Cam.jejun5(SEQ ID NO:159) 0 ~TTTATGAGAGTTTGATCCTGGCTCAGAGTGAACGCTGGCGGCCTGCTTAATACATGCA
Stp.aureus(SEQ ID NO:160) 0 ..TTTATGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCCTGCTTAATACATGCA

AGAGTTTGATCCTGGCTCAG
GGCGGACGGG

ER10 (SEQ ID NO:152)
E.colirre
Cam.jejun5
Stp.aureus
60 AGTCGAACGGTAACAG-----GAAGAAGCTTGCTTCTTT-----GCTGACGAGTGGCGGACGGG
62 AGTCGAACGAT-----GAAGCTTCTAGCTTGCTAGAAAGTGA-----TTAGTGGCGCACGGG
61 AGTCGAGCGAA-----CGGACGAGAAGCTTGCTTCTCTGATG-----TT-AGCGGCGGACGGG

TGAGTAA
ER10
E.colirre
Cam.jejun5
Stp.aureus
114 TGAGTAATGTCTGGGA-AACTGCCCTGATGGAGGGGATACTACTGGAACGGTAGCTAATA
114 TGAGTAAGGTATAGTTAATCTGCCCTACACAGAAGGACCAACAGTTGGAACGACTGCTAATA
113 TGAGTAACACGCTGGATAACCTAACCTATAAGACTGGGATAACTTCGGAAACCGAGCTAATA

E.colirre
Cam.jejun5
Stp.aureus
175 CCGCATAC-----GTCGCAAGAC-----CAAAGAGGGGGACCTTCG-GGCCCTTG
176 CTCTATACCTCTGCTTAACACACAAGTTGAGTAGG-GAAAG-----TTTTT-----CG
175 CCGGATAATATTTTGAACCCGATGTTCAAAAGTGAAAGACGGT----CTT----GCTGTCA

E.colirre
Cam.jejun5
Stp.aureus
221 CCATCGGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGTAACGGCTCACCTAGGCGACGA
221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGGTAATGGCTTACCAAGGCTATGA
229 CTTATAGATGATCCGCGCTGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGA

E.colirre
Cam.jejun5
Stp.aureus
283 TCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACCTGAGACACACGGTCCAGACTCCTA
283 CGCTTAAGCTGGTCTGAGAGGATGATCAGTCACACTGGAACCTGAGACACACGGTCCAGACTCCTA
291 TACGTAGCCGACCTGAGAGGGGTGATCGGCCACACTGGAACCTGAGACACACGGTCCAGACTCCTA
ACTCCTA
1659(COMPL)

```

FIG. 89A

E.colirrSE	345	CGGGAGGCAGCAGTGGGGAATATTGCCAATGGGCGGCAAGCCTGATGCAGCCATGCCGGGTG
Cam.jejun5	345	CGGGAGGCAGCAGTAGGGAATATTGCCAATGGGGAACCCCTGACGCAGCAACGCCGGGTG
Stp.aureus	353	CGGGAGGCAGCAGTAGGGAATCTCCGCAATGGCGAAAGCCTGACGGAGCAACGCCGGGTG
1659(COMPL)		CGGGAGGCAGCAG
E.colirrSE	407	TATGAAGAAGGCCCTTCGGGTTGTAAAGTACTTTTCAGCGGGGAGGAA-GGAGTAAAGTTAAT
Cam.jejun5	407	GAGGATGACACTTTTCGGAGCGTAACCTCCTTTCTTAGGGAAAG-----AATT
Stp.aureus	415	AGTGATGAAGGCTTCGGATCGTAAAACTCTGTTATTAGGGAAGACATATGTAGTAAC
E.colirrSE	468	ACCTTTGCTCATTGACGTTACCCGAGAGAAGCACCCGGCTAACTCCGTGCCAGCAGCCGGC
Cam.jejun5	455	C-----TGACGGTACCCTAAGGAATAAGCACCCGGCTAACTCCGTGCCAGCAGCCGGC
Stp.aureus	476	_TGTGCACATCTTGACGGGTACCTAATCAGAAAGCCACGGGCTAACTACGTGCCAGCAGCCGGC

FIG. 89B



E. coli irsE	530	GTAATACGGAGGGGTGCCAAGCGTTAATCGGAATTACTGGGGCGTAAAGCCGACCGAGGGCGTTT
Cam. jejuns	506	GTAATACGGAGGGGTGCCAAGCGTTACTCGGAATCACTGGGGCGTAAAGGGCGCGTAGGGGATT
Stp. aureus	538	GTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGGCGTAAAGCGCGGTAGGGGTTT
E. coli irsE	592	GTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACCTGCATCTGATACTGGCAAGCTT
Cam. jejuns	568	ATCAAGTCTCTTGTGAAATCTAATGGCTTAACCATTAACCTGCTTGGAACCTGATAGTCTA
Stp. aureus	600	TTAAGTCTGATGTGAAAGCCCAAGGCTCAACCGTGGAAGGTCATTGGAAACTGGAAACTT
E. coli irsE	654	GAGTCTCGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCCGTAGAGATCTGGAGGA
Cam. jejuns	630	GAGTGAGGGGAGAGGCGAGATGGAATTGGTGGTGTAGGGGTAAAAATCCGTAGATATCACCAAGA
Stp. aureus	662	GAGTGCAAGAGAGGAAAGTGAATTCCATGTGTAGCGGTGAAATGCCGAGAGATATGGAGGA
E. coli irsE	716	ATACCGGTGGCGAAGGCGGCCCCCTGGACGAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA
Cam. jejuns	692	ATACCCATTGCGAAGGCGGATCTGCTGGAACCTCAACTGACGCTAAGGCGCGAAAGCGTGGGGA
Stp. aureus	724	ACACCAGTGGCGAAGGCGACTTCTGTGCTGTAACTGACGCTGATGTGCGAAAGCGTGGGGA
E. coli irsE	778	GCAAAACAGGATTAGATACCCCTGGTAGTCCACGCGCGTAAACGATGTCGACTTGAGGTTGTGC
Cam. jejuns	754	GCAAAACAGGATTAGATACCCCTGGTAGTCCACGCGCGTAAACGATGTACACTAGTTGTTGGGT
Stp. aureus	786	TCAAACAGGATTAGATACCCCTGGTAGTCCACGCGCGTAAACGATGAGTGCTAAGTGTAGGGG

FIG. 89C

E.colirrfE	840	C-CTTGA-GCCGTGGCTTCCGGAGCTAACCGCGTTAAGTCGACCGCCCTGGGGAGTACGGCCG
Cam.jejun5	816	G-CTAGT-CATCTCAGTAATGACGCTAACCGCATTAAGTGACCGCCCTGGGGAGTACGGTCC
Stp.aureus	848	GT-TTCCGCCCTTAGTGCTGCAGCTAACCGCATTAAGCACTCCGCCCTGGGGAGTACGACCGC
E.colirrfE	900	AAGGTTAAAACTCAAATGAATTGACGGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTAATT
Cam.jejun5	876	AAGATTAAAACTCAAAGGAATAGACGGGGGACCCCGCACAAAGCGGTGGAGCATGTGGTTAATT
Stp.aureus	909	AAGGTTGAAACTCAAAGGAATTGACGGGGGACCCGCACAAAGCGGTGGAGCATGTGGTTAATT
E.colirrfE	962	CGATGCCAACGGCGAAGAACCCTTACCCTGGTCTTGACATCCACGGGAAGTTTTCAGAGATGAGAAT
Cam.jejun5	938	CGAAGATACGGCGAAGAACCCTTACCCTGGGCTTGATATCCTAAGAACCCTTTAGAGATAAGAGG
Stp.aureus	971	CGAAGCAACGGCGAAGAACCCTTACCCTTGACATCCTTTGACCACTCTAGAGATAGAGCC
E.colirrfE	1024	GTG--CCTTCGGG--AA-CCGTGAGACAGGTGCTGCATGGCTGTGTCAGCTCGTGTGTGA
Cam.jejun5	1000	GTGCTAGCTTGCTAGAA-CTTAGAGACAGGTGCTGCACGGCTGTGTCAGCTCGTGTGTGA
Stp.aureus	1033	TTCC-CCTTCGGG--GGACAAAGTGACAGGTGCTGCATGGTGTGTCAGCTCGTGTGTGA
SB-1		GCAACGAGCGCAACCC
E.colirrfE	1081	AATGTTGGGTTAAGTCCCCGCAACGAGCGCAACCCCTTATCCTTTGTTGCCAGCGGTCCGG-CC
Cam.jejun5	1061	GATGTTGGGTTAAGTCCCCGCAACGAGCGCAACCCACGTAATTAAGTTGCTAACGGTTCGG-CC
Stp.aureus	1092	GATGTTGGGTTAAGTCCCCGCAACGAGCGCAACCCCTTAAGCTTAGTTGCCATCA-TTAAGT-T

FIG. 89D

SB-3 (SEQ ID NO:157)		ATGACGTCAGTCAATC
SB-4 (SEQ ID NO:154)		ATGACGTCAGTCAATC
E.coli rrse	1142	GGGAACCTCAAAGGAGACTGCCAGTGATAACTGGAGGAAGGTGGGGATGACGTCAGTCAATC
Cam. jejuns	1122	GAGCACTCTAAATAGACTGCCCTTCG-TAAGGAGGAGGAAGGTGTGGACGACGTCAGTCAATC
Stp. aureus	1152	GGGCACTCTAAGTTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAGTCAATCATC
SB-3		ATGCCCCCTTA
SB-4		ATGCCCCCTTACGA
E.coli rrse	1204	ATGCCCCCTTACGACCAGGGCTACACACCGTGCTACAATGGCGCATACAAAGAGAGCGACCTC
Cam. jejuns	1183	ATGCCCCCTTATGCCAGGGCGACACACGCTGCTACAATGGCATATAGAAATGAGACGCAATACC
Stp. aureus	1214	ATGCCCCCTTATGATTGGGCTACACACGCTGCTACAATGGACAATACAAAGGGCAGCGAAACC
E.coli rrse	1266	GCGAGAGCAAGCGGACCTCATAAAGTGCGTGTAGTCCGGATTGGAGTCTGCAACTCGACTC
Cam. jejuns	1245	GCGAGGTGGAG-CAAATCTATAAAATATGTCCAGTTCGGATTGTCTCTGCAACTCGAGAG
Stp. aureus	1276	GCGAGGTCAAAGCAAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTA
E.coli rrse	1328	CATGAAGTCGGAATCGCTAGTAATCGTGATCAGA-ATGCCACGGTGAATACGTTCCCGGGC
Cam. jejuns	1306	CATGAAGCCGGGAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCGGGT
Stp. aureus	1338	CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCGGGT
1743 (compl)		CGGTGAATACGTTCCCGGGC

FIG. 89E

E. coli irsE	1389	CTGTACACACCCGCGCTCACACCATGGGAGTGGGTTGCCAAAAGAAGTAGGTTAACCT
Cam. jejuni	1368	CTGTACTCACCGCGCGTACACCATGGAGTTGATTTCACCTGGAAGCCGGAATACT--A-A
Stp. aureus	1399	ATTGTACACACCGCGCTCACACACGAGAGTTGTAAACACCCGAAGCCGGTGAGTAACCT
1743 (compl)		CTGTAC
E. coli irsE	1451	TCG- <u>GGAGGGCGCTTACCACTTTGTGATTCA</u> TGACTGGGGTGAAGTCGTAACAAGGTAACCG
Cam. jejuni	1427	AC- <u>-T-AGTTACCGTCCACAGTGGAA</u> TACGCGACTGGGGTGAAGTCGTAACAAGGTAACCG
Stp. aureus	1461	TTAGGAGCTAGCCGTCGAAGGTGGGACAAATGATTGGGGTGAAGTCGTAACAAGGTAACCG
E. coli irsE	1512	TAGGGGAACCTGCGGTTGGATCACCTCCTTA---
Cam. jejuni	1485	TAGGAGAACCCTGCGGTTGGATCACCTCCT----
Stp. aureus	1523	TATCGGAAGGTGCGGCTGGATCACCTCCTTCT-

FIG. 89F

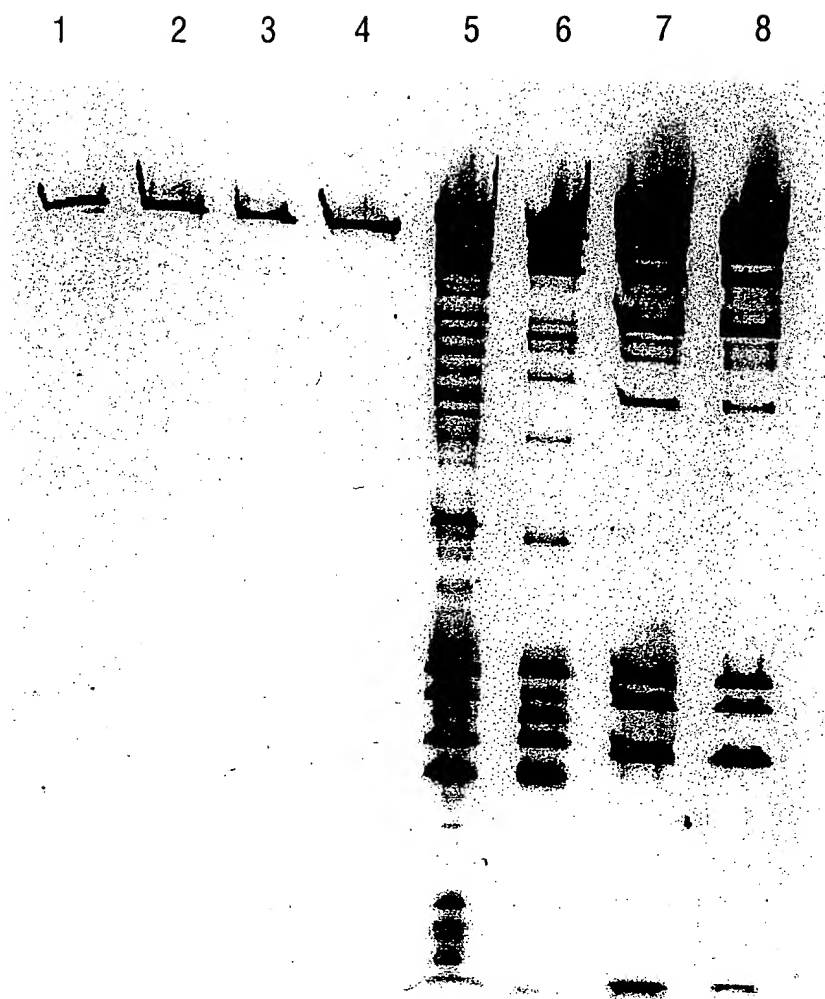


FIG. 90

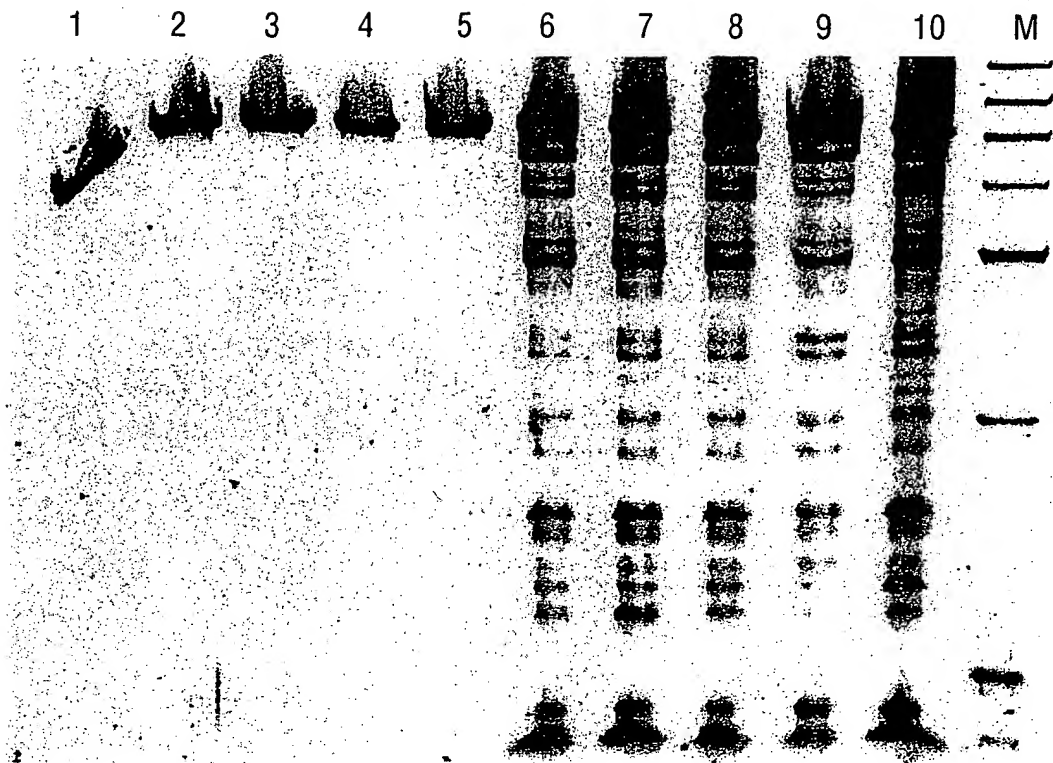


FIG. 91A

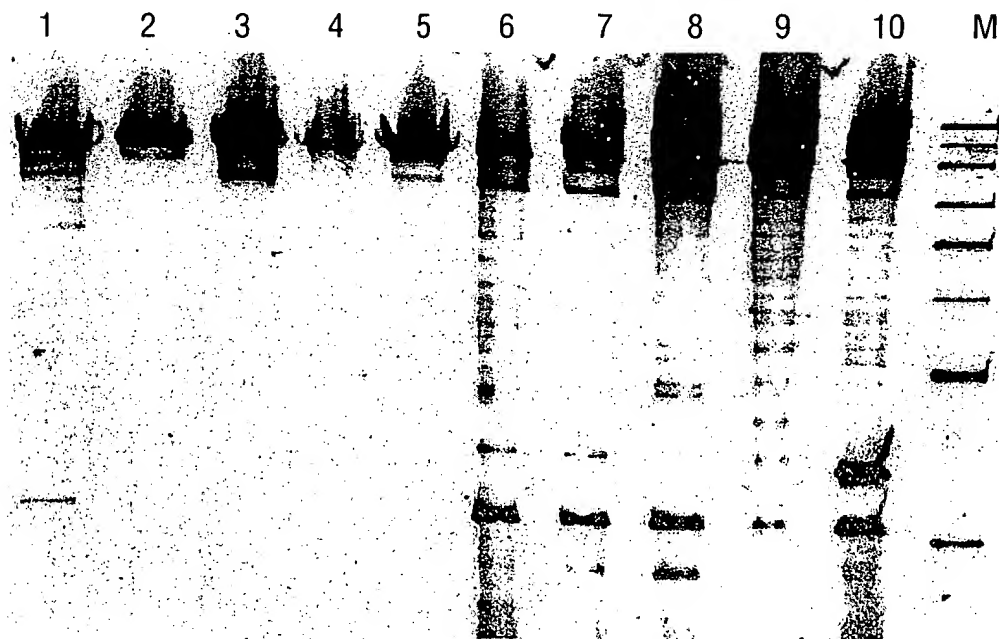
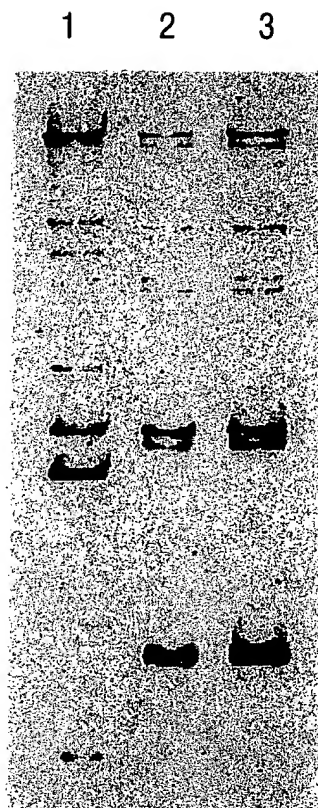


FIG. 91B



**FIG. 92**

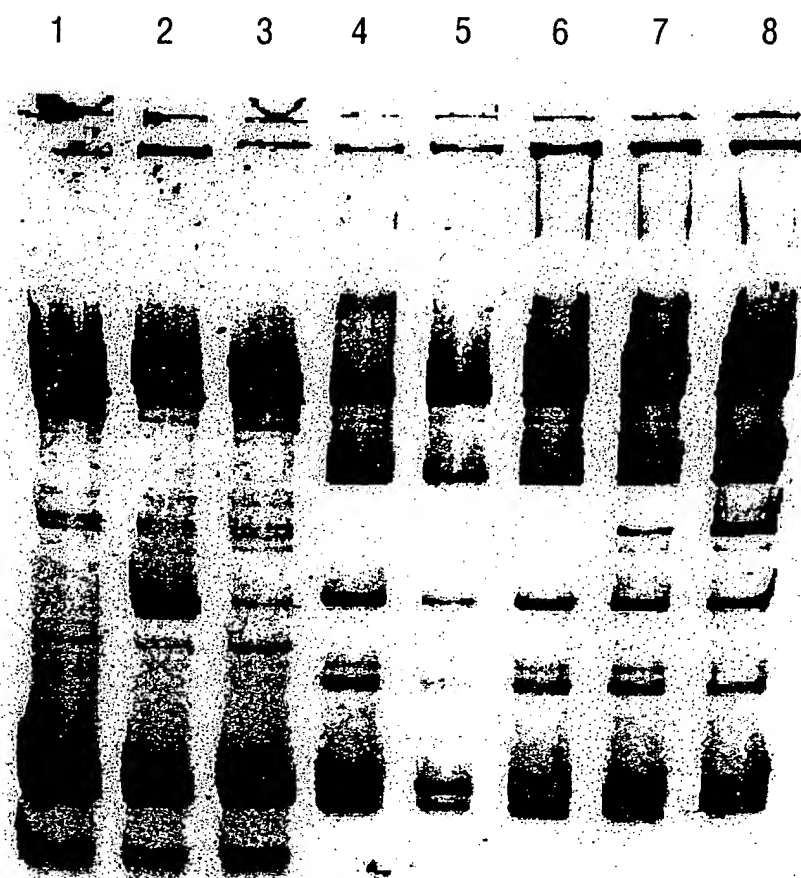


FIG. 93



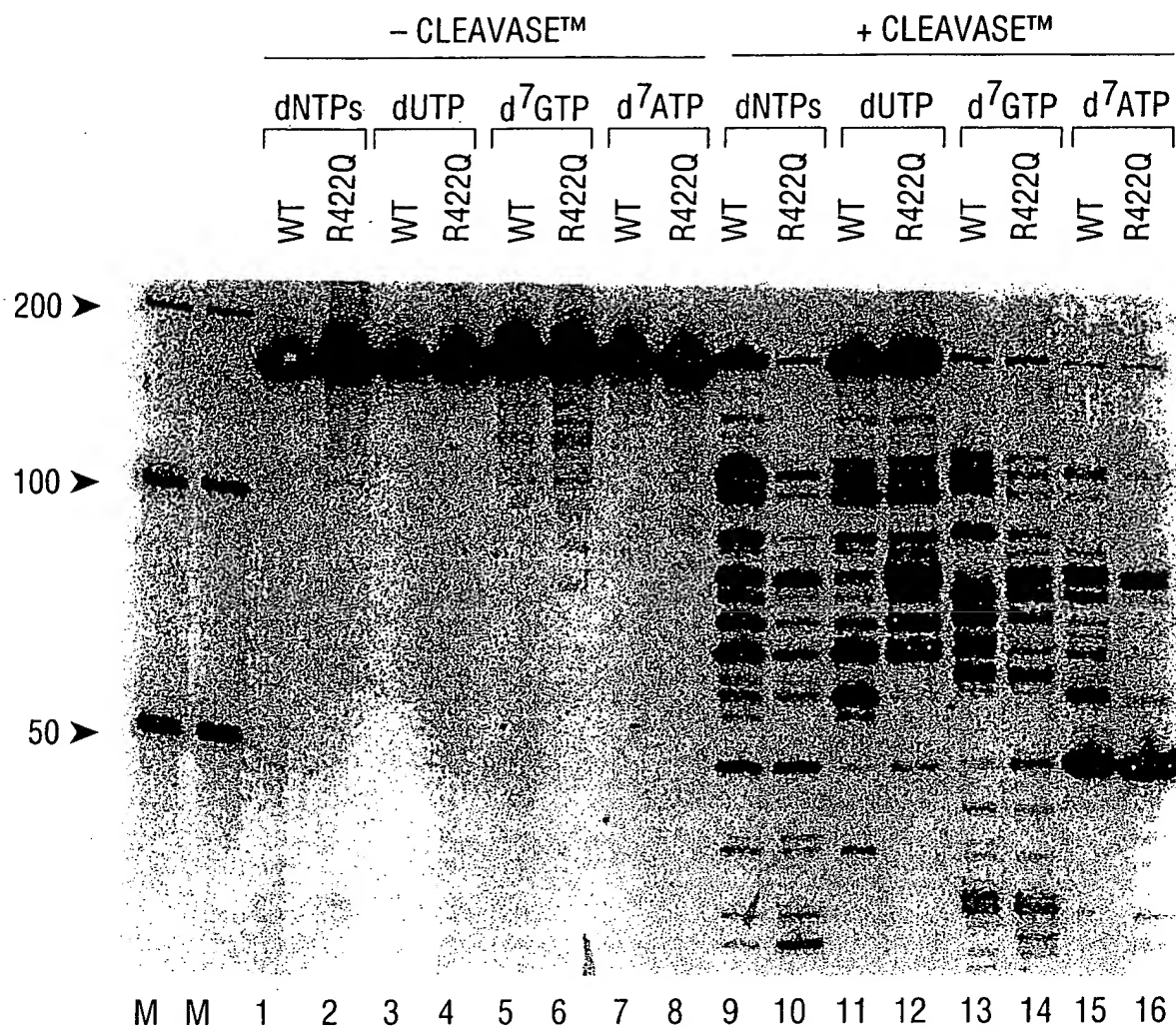


FIG. 94

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